

**Part 1:** **TITLE, AUTHORS, APPROVALS, etc**

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| **Code assigned:** | **2020.184B** |  |
| **Short title:** Create one new genus (*Yonseivirus*) including three new species (*Caudovirales*: *Siphoviridae*) | | |
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**Author(s) and email address(es)**

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| Andrew Kropinski |

**List the ICTV Study Group(s) that have seen this proposal**

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| *Caudovirales* Study Group, Bacterial and Archaeal Viruses Subcommittee |

**ICTV study group comments and response of proposer**

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**Authority to use the name of a living person**

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| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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| Date first submitted to SC Chair | June 2020 |
| Date of this revision (if different to above) |  |

**ICTV-EC comments and response of the proposer**

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

**Name of accompanying Excel module**

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| 2020.184B.R.Yonseivirus.xlsx |

**Abstract**

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| We have created a new genus of *Klebsiella* phages, *Yonseivirus*, which is peripherally related to the genus *Chivirus*. |

**Text of proposal**

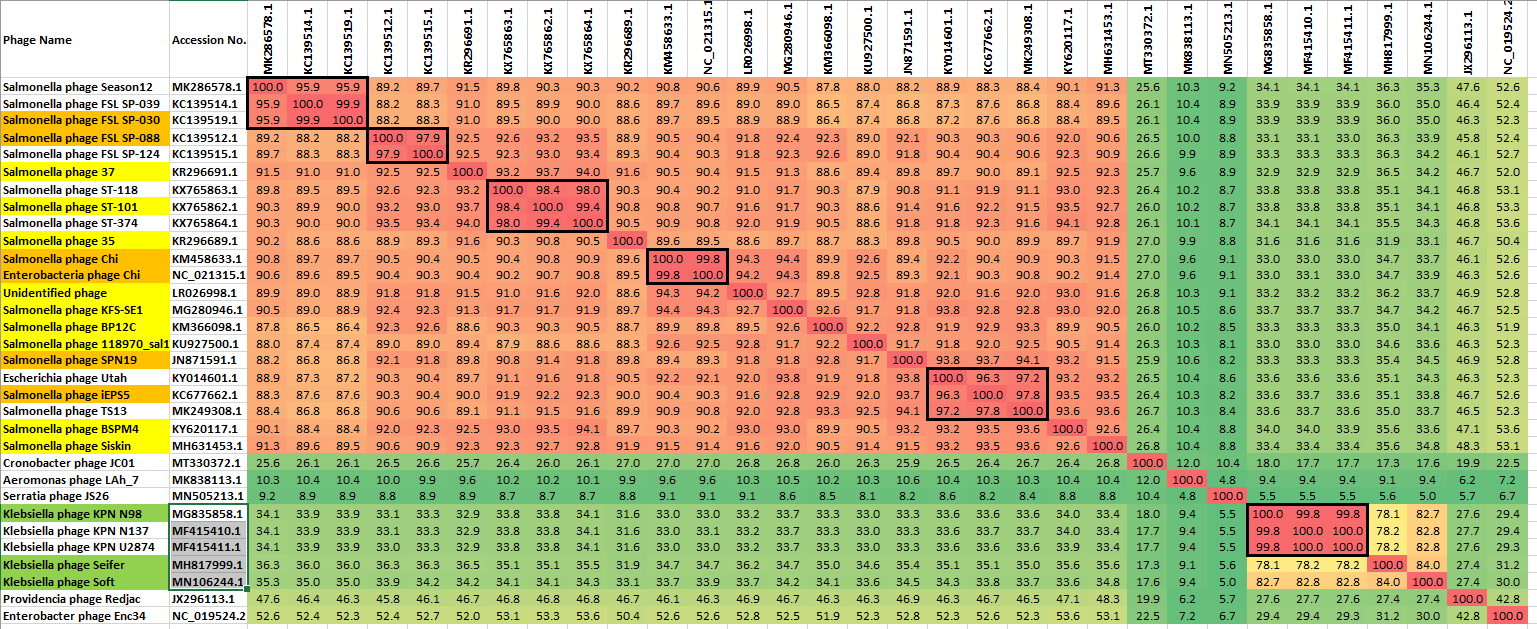
|  |  |
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| |  | | --- | | **Species demarcation criteria:** We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm. | |

**Supporting evidence**

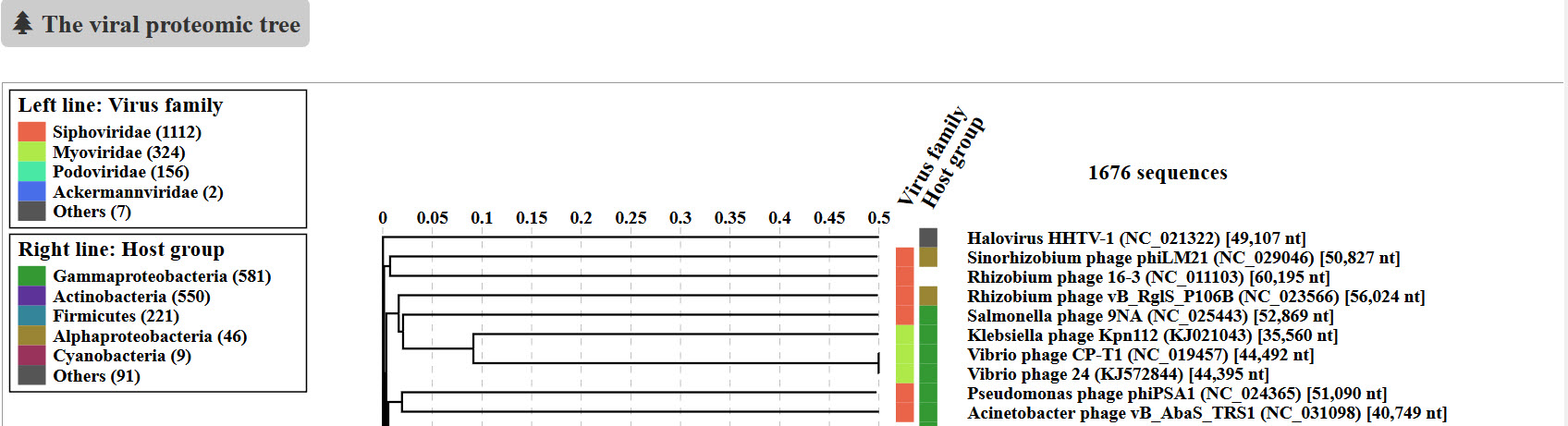
**Source of the name of this taxon:** This genus is named after Yonsei University (Korea) where, in 2017, Klebsiella phage KPN N137 was isolated in the College of Medicine.

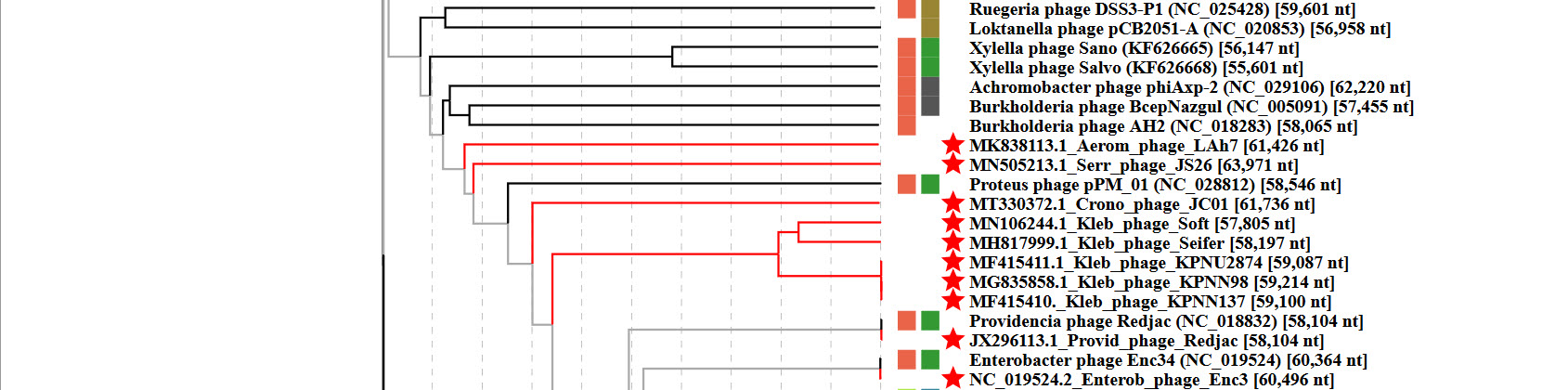
**History:** These lytic phages where initially isolated and characterized in South Korea, though no publications have appeared. Two related species Klebsiella phage Soft (MN106244) and Klebsiella phage Seifer (MH817999) [Salazar AJ et al. 2019] were isolated in Texas (USA). These were characterized as possessing 12 nt cos end 5' overhang sequences. The authors commented on their relationship to Salmonella phage Chi (*Chivirus*).

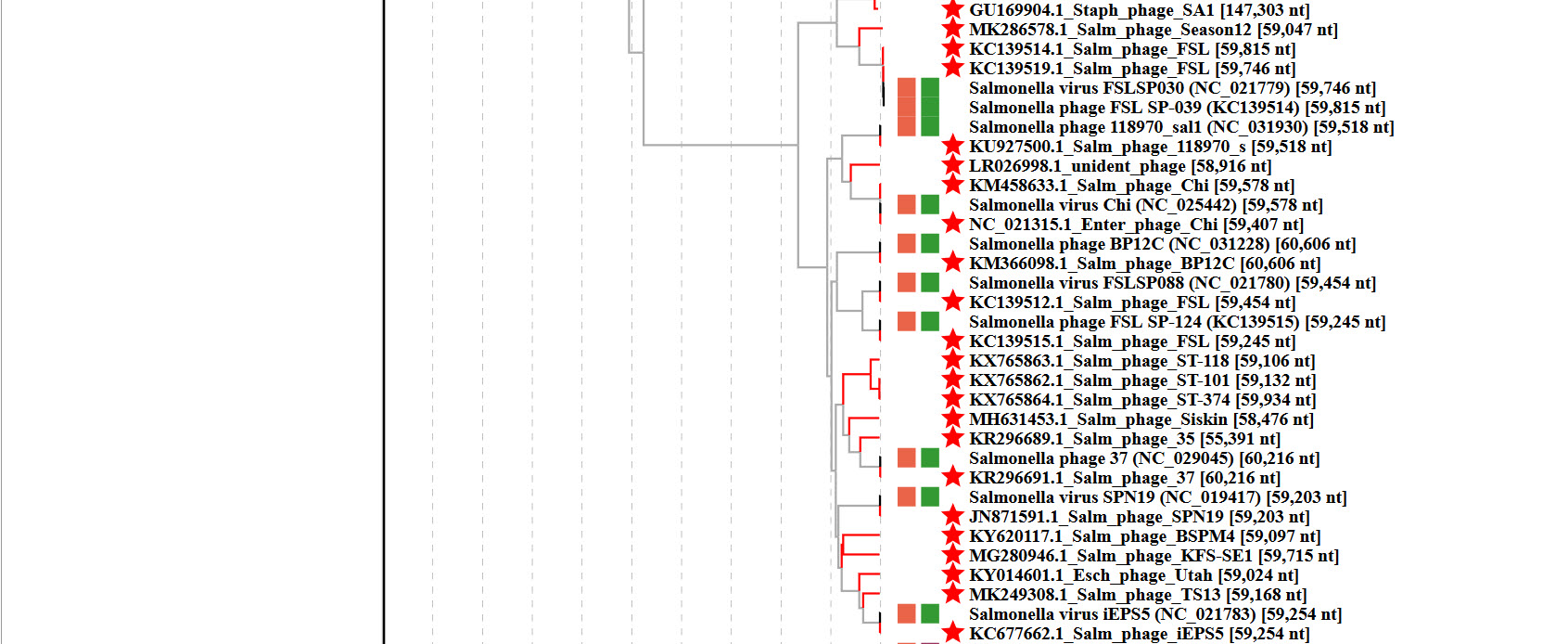
**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [1]) computes pairwise intergenomic distances/similarities amongst phage genomes. The black box delineates strains. The phage names highlighted in **light green** are new species within the genus *Yonseivirus*.

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**ViPTree analysis:** ViPTree analysis (<https://www.genome.jp/viptree/>; [2]) is based upon Rohwer and Edwards (2002) Phage Proteomic Tree [3]. The large **blue arrowhead** points to the *Yonseivirus* genus while the large **red arrowhead** points to a potential family which would include *Chivirus*.

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**Specific Reference:**

Salazar AJ, Lessor L, O'Leary C, Gill J, Liu M. Complete Genome Sequence of *Klebsiella pneumoniae* Siphophage Seifer. Microbiol. Resour. Announc. 2019;8(46):e01289-19. Published 2019 Nov 14. doi:10.1128/MRA.01289-19 [Seifer]

**GenBank Summary:**

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| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNAs | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Klebsiella phage KPN N137 | [MF415410.1](https://www.ncbi.nlm.nih.gov/nuccore/MF415410.1) | 59.1 | 56.3 | [79](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63782/466403|Klebsiella phage KPN N137/viral segment/) | 0 | 100 | 100 |
| Klebsiella phage Seifer | [MH817999.1](https://www.ncbi.nlm.nih.gov/nuccore/MH817999.1) | 58.2 | 56.1 | [82](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/72983/412468|Klebsiella phage Seifer/viral segment/) | 0 | 78.2 | 87.3 |
| Klebsiella phage Soft | [MN106244.1](https://www.ncbi.nlm.nih.gov/nuccore/MN106244.1) | 57.81 | 55.9 | [87](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/84249/679218|Klebsiella phage Soft/viral segment/) | 0 | 82.8 | 88.6 |

**(\*) Determined from VIRIDIC results [1]**

**(\*\*) Determined using CoreGenes 3.5 at http://binf.gmu.edu:8080/CoreGenes3.5/ [6]**

**N.B. Klebsiella phages KPN N98 (**[MG835858.1](https://www.ncbi.nlm.nih.gov/nucleotide/MG835858.1?report=genbank&log$=nucltop&blast_rank=3&RID=F912B7KV014)) **and KPN U2874 (**[MF415411.1](https://www.ncbi.nlm.nih.gov/nucleotide/MF415411.1?report=genbank&log$=nucltop&blast_rank=2&RID=F912B7KV014)) **should be considered strains of *Klebsiella virus N137.***

**Electron micrograph:** None available

**References**

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