

**PROPOSAL Prokaryote SC**  
**New species 'Enterobacteria phage HK022'**  
**in Genus 'λ-like viruses'**

**2002.135B.02** to designate *Enterobacteria phage HK022* as a Species of the Genus λ-like viruses

**Rationale**

Bacteriophage HK022 is closely related to the type species of this genus (bacteriophage ) by the criteria that it shares the same functional order of genes and that many of its sequences are closely related to the corresponding sequences of . HK022 and share the same host (*Escherichia coli*) and the same temperate life style.

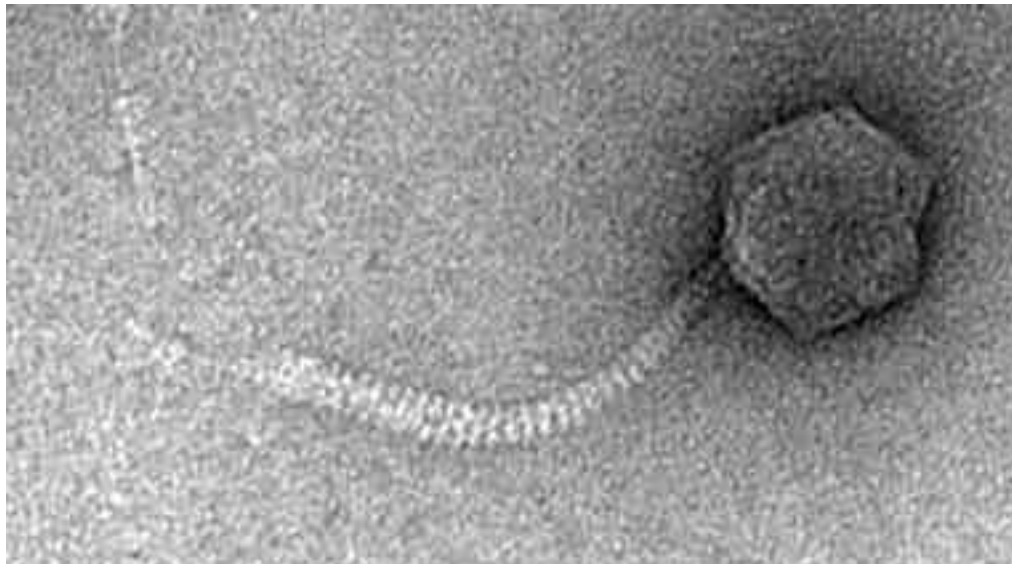
**Distinguishing properties**

The DNA replication genes and the generalized recombination genes of HK022 are more closely related to the corresponding genes of bacteriophage P22 than to those of . The head genes of HK022 are not detectably related by sequence to those of but are nearly identical in sequence to those of bacteriophage HK97, another [proposed] species of the Genus 'λ-like viruses'. The major capsid subunit of HK97 becomes covalently linked into the 'chainmail' topology during capsid maturation, like HK97 but unlike . HK022 has different immunity from .

**Virion properties**

*Morphology*

Phage heads are icosahedral with a triangulation number of 7, and 60 nm in diameter. Tails are non-contractile, flexible, measure 135 x 8 nm, and have short brush-like terminal fibers.



*Nucleic acid*

The genome in the virion is a linear, non-permuted molecule of 40,751 bp, with 10 base 3' extensions (cos ends). The complete genome sequence is known.

#### *Proteins*

The major head subunit is found in the virion covalently crosslinked to its neighbors in the 'chainmail' topology. The amino acid sequence of the major head protein is identical to that of phage HK97 and so presumably shares the same structure. Tail proteins are similar to those of the type species.

#### *Lipids*

None reported.

#### *Carbohydrates*

None reported.

### **Genome organization and replication**

There are approximately 69 protein coding genes that occupy 90% of the genomic DNA sequence. Gene orientation and order along the map are essentially like those of the type species, as are the patterns of transcription. There are also high levels of similarity of sequence (and presumably function) for the site-specific recombination genes, the lysis genes, and the late transcription regulator ('Q') genes. There is modest sequence similarity over about 2/3 of the tail gene region.

### **References**

Dhillon, T.S. & Dhillon, E.K. (1976). Temperate coliphage HK022. Clear plaque mutants and preliminary vegetative map. *Jpn. J. Microbiol.* **20**, 385-396.

Juhala, R.J., Ford, M.E., Duda, R.L., Youlton, A., Hatfull, G.F. and Hendrix, R.W. (2000) Genomic sequences of bacteriophages HK97 and HK022: pervasive genetic mosaicism in the lambdoid bacteriophages, *J. Mol. Biol.* **299** 27-52.

Weisberg, R.A., Gottesman, M.E., Hendrix, R.W. and Little, J.W. (1999) Family values in the age of genomics: comparative analyses of temperate bacteriophage HK022, *Ann. Rev. Genet.* **33**, 565-602.