

**PROPOSAL from the Prokaryote SC:  
New species 'Enterobacteria phage HK97'  
in Genus 'λ-like viruses'**

**2002.133B.02** to designate *Enterobacteria phage HK97* as a Species of the Genus λ-like viruses

### **Rationale**

Bacteriophage HK97 is closely related to the type species of this genus (bacteriophage λ) 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 λ. HK97 and λ share the same host (*Escherichia coli*) and the same temperate life style.

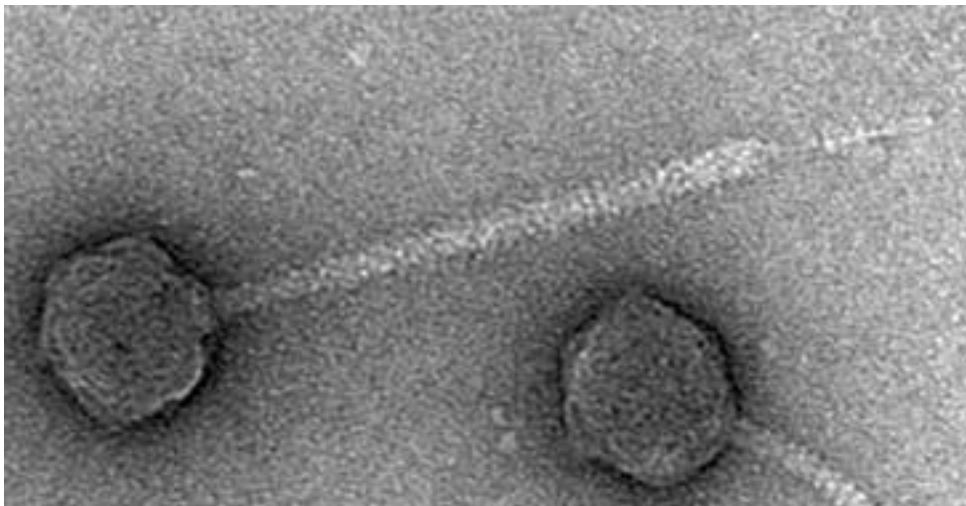
### **Distinguishing properties**

The DNA replication genes and the generalized recombination genes of HK97 are more closely related to the corresponding genes of bacteriophage P22 than to those of λ. The head genes of HK97 are not detectably related by sequence to those of λ but are nearly identical in sequence to those of bacteriophage HK022, 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 HK022 but unlike λ.

### **Virion properties**

#### *Morphology*

Phage heads are icosahedral with a triangulation number of 7 and 60 nm in diameter. Tails are non-contractile, flexible, measure 180 x 8 nm, and have short brush-like terminal fibers.



*Nucleic acid*

The genome in the virion is a linear, non-permuted molecule of 39,732 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 high resolution structure of the head is known and reveals a novel fold, which however is probably shared with most and perhaps all of the tailed phages. Tail proteins are similar to those of the type species.

#### *Lipids*

None reported.

#### *Carbohydrates*

None reported.

### **Genome organization and replication**

There are approximately 65 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. HK97 and are homoimmune; this correlates with the near identity of their *ci* and *cro* repressor genes and the flanking operators. 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**

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