Taxonomic proposal to the ICTV Executive Committee



This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections).

Code(s) assigned:	2008.081B	(to be completed by ICTV officers)			
Short title: Create new species named Enterobacteria phage K1-5 in the genus "SP6-like viruses", subfamily Autographivirinae, family Podoviridae (e.g. 6 new species in the genus <i>Zetavirus</i> ; re-classification of the family <i>Zetaviridae</i> etc.) Modules attached [Please check all that apply): [Please check all that apply]: [Please check all that					
Author(s) with e-mail address(es) of the proposer:					
Ian J. Molineux molineux@mail.utexas.edu					
ICTV-EC or Study Group comments and response of the proposer:					

MODULE 5: NEW SPECIES

Code 2008.081B		(assigned by ICTV officers)	
To create new species assigned as follows: Fill in all that apply. Ideally, species assigned as follows:			
Genu	is: "SP6-like viruses"	should be placed within a genus, but it is	
Subfamil	y: Autographivirinae	acceptable to propose a species that is within a Subfamily or Family but not	
Famil	y: Podoviridae	assigned to an existing genus (in which	
Orde	er: Caudovirales	case put "unassigned" in the genus box)	

Name(s) of proposed new species:

Entanahaataria nhaga V15	-	
Enterobacteria phage K1-5		

Argument to justify the creation of the new species:

If the species are to be assigned to an existing genus, list the criteria for species demarcation and explain how the proposed members meet these criteria.

Phage K1-5 was first described in 2001 as having dual host-specificity, growing on both K1 and K5 capsulated strains of *Escherichia coli*. Morphologically, K1-5 belongs to the family *Podoviridae*. The phage codes for its own RNA polymerase and thus should be assigned to the subfamily *Autographivirinae*. The K1-5 genome, containing 44385 bp, is ~700 bp larger than SP6, the phage most closely related (NC 008152). The promoter specificity of K1-5 RNA polymerase is different from that of SP6 and the host ranges of the two phages do not overlap. Host range is primarily determined by two heaxameric sets of phage-coded tailspike enzymes with specificities for distinct polysaccharide capsules.

References:

Scholl, D., S. Rogers, S. Adhya, and C. Merril. 2001. Bacteriophage K1-5 encodes two different tail fiber proteins, allowing it to infect and replicate on both K1 and K5 strains of *Escherichia coli*. J. Virol. 75:2509-2515.

Scholl, D., J. Kieleczawa, P. Kemp, J. Rush, C. C. Richardson, C. Merril, S. Adhya, and I. J. Molineux. 2004. Genomic analysis of bacteriophages SP6 and K1-5, an estranged subgroup of the T7 supergroup. J. Mol. Biol. 335:1151-1171.

Annexes:

Include as much information as necessary to support the proposal. The use of Figures and Tables is strongly recommended.