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:	***2008.040B***	(to be completed by ICTV officers)

Short title: addition of an new species HK620 within genus 'the P22-like viruses'
(e.g. 6 new species in the genus *Zetavirus*; re-classification of the family *Zetaviridae* etc.)

Modules attached (please check all that apply):	**1** ☐	**2** ☐	**3** ☐	**4** ☐	**5** ☒	**6** ☐	**7** ☐		

Author(s) with e-mail address(es) of the proposer:

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ICTV-EC or Study Group comments and response of the proposer:

MODULE 5: **NEW SPECIES**

Code	***2008.040B***	(assigned by ICTV officers)

To create new species assigned as follows:

Genus:	***The P22-like viruses***
Subfamily:	
Family:	***Podoviridae***
Order:	***Caudovirales***

Fill in all that apply. Ideally, species should be placed within a genus, but it is acceptable to propose a species that is within a Subfamily or Family but not assigned to an existing genus (in which case put "unassigned" in the genus box)

Name(s) of proposed new species:

Salmonella phage HK620

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.

The genome of a temperature-sensitive clear-plaque mutant HK620 consists of 38,297 nucleotides in which we recognize 60 open reading frames (orfs). Eighteen of these lie in a region of the genome that we call the virion structure domain. The other 42 orfs lie in what we call the metabolic domain.Virions of HK620 resemble those of phage P22. The virion structural orfs encode three kinds of putative proteins relative to the virion proteins of P22: (1) those that are nearly (about 90 %) identical; (2) those that are weakly (about 30 %) identical; and (3) those composed of nearly and weakly identical segments. We hypothesize that these composite proteins form bridges between the virion proteins of the other two kinds.

The putative transcriptional regulatory gene circuitry of HK620 seems to resemble that of *Siphoviridae* phage lambda. Integration, on the other hand, resembles that of satellite phage P4 in that the attP sequence lies between the leftward promoter and int rather than downstream of int.Comparing the metabolic domains of several lambdoid phage genomes reveals seven short conserved sequences roughly defining boundaries of functional modules.

References:

** Clark AJ, Inwood W, Cloutier T, Dhillon TS. (2001) Nucleotide sequence of coliphage HK620 and the evolution of lambdoid phages. J Mol Biol. 24;311(4):657-79.

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