



This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). For guidance, see the notes written in blue and the separate document "Help with completing a taxonomic proposal"

Please try to keep related proposals within a single document; you can copy the modules to create more than one genus within a new family, for example.

MODULE 1: **TITLE, AUTHORS, etc**

Code assigned:	2009.007a-fV	(to be completed by ICTV officers)			
Short title: Reptile paramyxoviruses: 1 new species and new genus, Ferlavirus (e.g. 6 new species in the genus <i>Zetavirus</i>)					
Modules attached (modules 1 and 9 are required)	1 <input checked="" type="checkbox"/>	2 <input checked="" type="checkbox"/>	3 <input checked="" type="checkbox"/>	4 <input type="checkbox"/>	5 <input type="checkbox"/>
	6 <input type="checkbox"/>	7 <input type="checkbox"/>	8 <input type="checkbox"/>	9 <input checked="" type="checkbox"/>	

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

Gael Kurath (gkurath@usgs.gov)

Has this proposal has been seen and agreed by the relevant study group(s)?
Please select answer in the box on the right

Yes

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

Date first submitted to ICTV:

May 10th, 2009

Date of this revision (if different to above):

MODULE 2: **NEW SPECIES**

Part (a) to create and name one or more new species.

If more than one, they should be a group of related species belonging to the same genus (see Part b)

Code	2009.007aV	(assigned by ICTV officers)
To create 1 new species with the name(s):		
<i>Fer-de-Lance paramyxovirus</i>		

Part (b) assigning new species to higher taxa

All new species must be assigned to a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	2009.007bV	(assigned by ICTV officers)
To assign the species listed in section 2(a) as follows:		
Genus:	<i>Ferlavirus (new)</i>	Fill in all that apply. <ul style="list-style-type: none"> If the higher taxon has yet to be created (in a later module, below) write "(new)" after its proposed name. If no genus is specified, enter "unassigned" in the genus box.
Subfamily:	<i>Paramyxovirinae</i>	
Family:	<i>Paramyxoviridae</i>	
Order:	<i>Mononegavirales</i>	

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
 - If species demarcation criteria (see module 3) have previously been defined for the genus, explain how the new species meet these criteria.
 - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

The only reptile virus currently in the family *Paramyxoviridae* is Fer-de-Lance virus (previously listed as FDLV, suggested here as FdIPV, for Fer-de-lance paramyxovirus), which is listed as an unassigned virus. It replicates at low temperatures as expected for a virus from a poikilothermic (cold-blooded) host. It has biological and molecular features consistent with being a member of the subfamily *Paramyxovirinae*, in the family *Paramyxoviridae*. This proposed species is distinct from all other established paramyxovirus species in having a reptile host, low replication temperatures, presence of a unique U gene between the N and P genes, and low levels of sequence identity with other known paramyxoviruses in the complete genome sequences available.

GenBank Numbers:

NC-005084 and AY141760 are full length FdIPV genome

AY534644 and AY534645 are U genes from isolates GonoGer85 and Biti-CA98

AY725422 is full length F gene from isolate GonoGer85

AF286043 through AF286046 are partial HN and L sequences from 2 isolates in Kindermann et al., 2001.

AF251500 is partial F sequence from a wild caught FdIPV

MODULE 3: **NEW GENUS**

creating and naming a new genus

Code	2009.007cV	(assigned by ICTV officers)
To create a new genus to contain the species listed below		

Code	2009.007dV	(assigned by ICTV officers)
To name the new genus: <i>Ferlavirus</i>		

assigning a new genus to higher taxa

Code	2009.007eV	(assigned by ICTV officers)
To assign the new genus as follows: Ideally, a genus should be placed within a higher taxon, but if not, write " unassigned " in the box below.		
Subfamily:	<i>Paramyxovirinae</i>	If any of these taxa has yet to be created (in module 4, 5 or 6) please write " (new) " after its proposed name.
Family:	<i>Paramyxoviridae</i>	
Order:	<i>Mononegavirales</i>	

assigning type species and other species to a new genus

Code	2009.007fV	(assigned by ICTV officers)
To designate the following as the type species of the new genus		
<i>Fer-de-lance paramyxovirus</i>		Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered
Code		(assigned by ICTV officers)
To assign the following as additional species of the new genus:		
)		

Reasons to justify the creation of a new genus:

Additional material in support of this proposal may be presented in the Appendix, Module 9

FdlPV occupies a host niche in reptile species and replicates at low temperatures: both of these features are distinct from known mammalian paramyxoviruses. Phylogenetic analyses indicate this species is on a long branch that is distinct from branches leading to known paramyxovirus genera or unassigned paramyxovirus species from mammalian hosts. See trees in module 9. It is also phylogenetically distant from fish paramyxoviruses (see module 9 of independent proposal for a new genus of paramyxoviruses from fish hosts).

Most important in distinguishing this virus from known paramyxoviruses is the presence of an additional gene not found in paramyxoviruses of any other genus. The complete genome sequence of FdlPV (Kurath et al., 2004) is 15,378 nt in length, with gene order 3' N-U-P-M-F-HN-L 5'. The unique U gene found in the FdlPV genome is expressed in infected cells, and it has been sequenced also from two additional snake paramyxovirus isolates Gono-Ger85 and Biti-CA98. The U gene is not present in any other paramyxoviruses characterized from mammalian hosts. The complete genome sequence of the fish paramyxovirus, Atlantic salmon paramyxovirus (AsaPV), shows that no U gene is present in this genome.

Demarcation criterion for this proposed genus thus include isolation from reptile hosts, ability to replicate at low temperatures, presence of a U gene between the N and P cistrons, and phylogenetic clustering with the type species FdlPV, separate from paramyxoviruses in other known genera.

Origin of the new genus name:

Sigla from the type strain name Fer-de-Lance Virus

Reasons to justify the choice of type species:

FdlPV was the first reptile paramyxovirus to be isolated and the complete genome of FdlPV has been determined.

Species demarcation criteria in the new genus:

- If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences of new species

For species demarcation see nt divergence levels described at end of module 2.

Genbank Accession numbers:
See end of module 2

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Clark et al., 1979. *Journal of general Virology* 44:405-418
Ahne et al., 1999 *Virus Research* 63:65-74.
Kindermann et al., 2001. *Archives of Virology* 146:1021-1035
Franke et al., 2001. *Virus Research* 80:67-74.
Kurath et al., 2004. *J. Virology* 78: 2045-2056

Annex:

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders.

The use of Figures and Tables is strongly recommended.

Fer-de-lance virus (FdIPV) and other paramyxoviruses from reptile hosts

FdIPV (listed as FDLV) is currently an unassigned virus in the family *Paramyxoviridae* (ICTV 8th report). There are no other reptile viruses currently listed in the family. Many paramyxoviruses have been isolated from snakes and other reptiles since FdIPV was first isolated in Switzerland in 1972. They cause respiratory disease and nervous symptoms in snakes in captive collections (zoos or venom farms), and paramyxovirus sequences have been found in RNA from wild snakes. There are many publications describing these viruses, and four papers that provide molecular data that can be used toward updating the ICTV chapter:

Ahne et al., 1999 *Virus Research* 63:65-74.

Partial HN (352 nt) and L (518 nt) gene sequences from 16 reptilian paramyxoviruses collected from 14 host species (all snakes except 1 lizard) between 1972-1998. Phylogenetic analysis identified 2 subgroups that differed by 20-22% at the nt level, and several intermediate sequences (including FdIPV). Authors suggested that the two subgroups, designated A and B, represented distinct species with multiple strains (less than 2.5% nt diversity within each subgroup, and 5-6 isolates within each subgroup). This designation will require additional sequence information on these viruses.

Kindermann et al., 2001. *Archives of Virology* 146:1021-1035.

Partial HN (679 nt) and L (627 nt) gene sequences from 2 additional snake paramyxovirus isolates. Phylogeny with sequences from Ahne 1999 showed one isolate was in B subgroup and the other was intermediate.

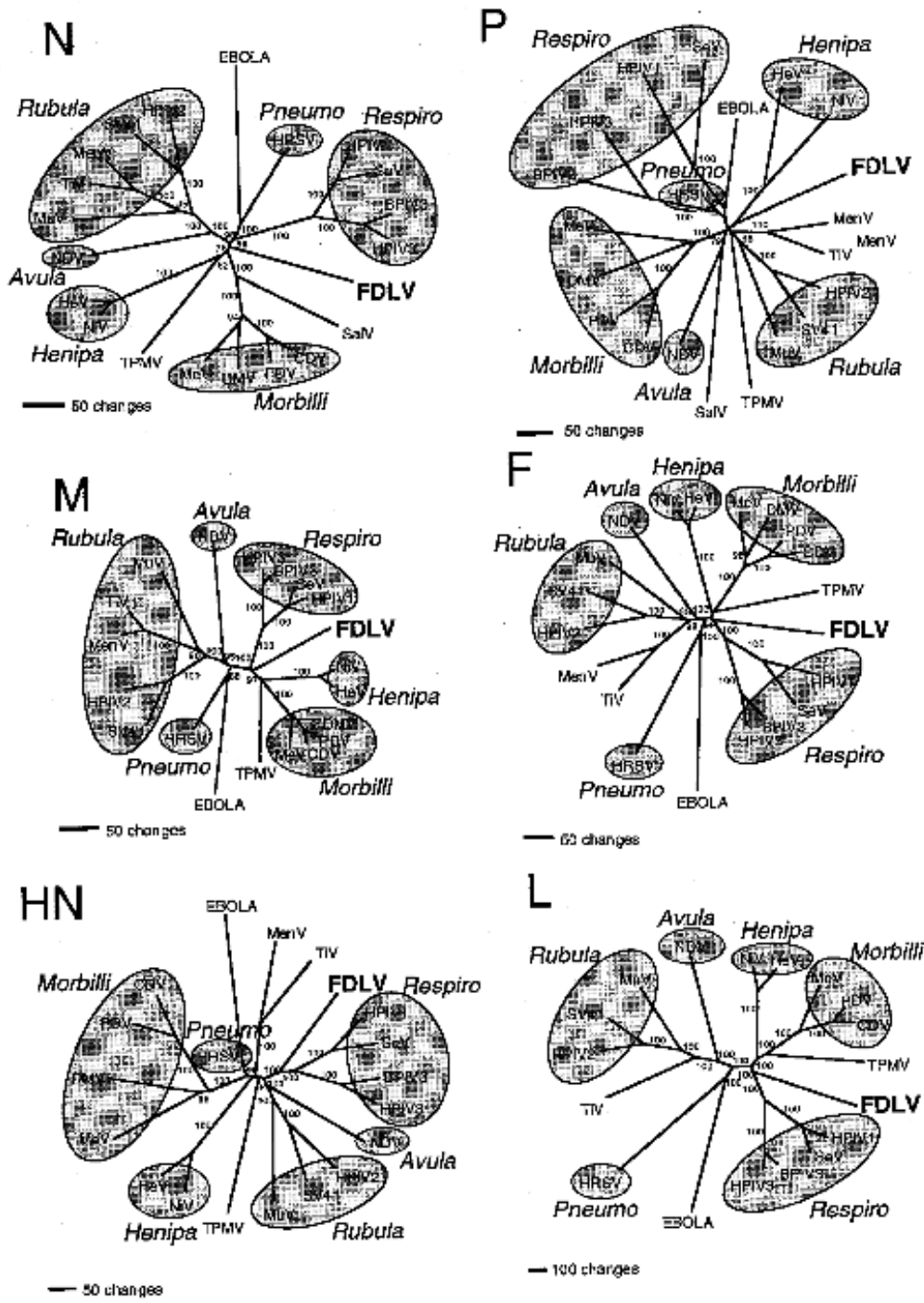
Franke et al., 2001. *Virus Research* 80:67-74.

Partial L (566 nt) and F (918 nt) gene sequences from 18 different snake paramyxovirus isolates (16 new and 2 characterized in Ahne 1999) collected in Germany between 1989-1999. F gene sequences showed identical conserved heptad repeat and furin cleavage sites distinct from other paramyxovirus type species. Suggests new genus.

Kurath et al., 2004. *J. Virology* 78: 2045-2056.

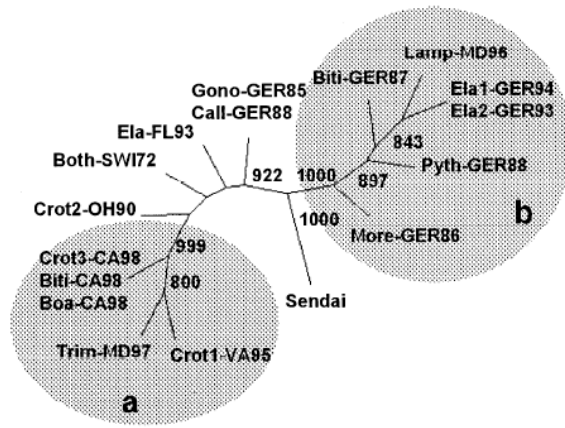
Complete genome sequence of FdIPV. Genome is 15,378 nt in length, with gene order 3' N-U-P-M-F-HN-L 5'. P gene editing is like *rubulavirus* genus, where mRNA encodes V protein and edited mRNA encodes P. Most significant finding is presence of the unique U gene

after the N gene - this is not seen in any other paramyxovirus. Role of the U gene/protein is unknown, but it is actively transcribed into mRNA in infected cells, and was shown to be present in two other snake viruses in Ahne et al. 1999. Phylogenetic analyses of all genes indicated FdIPV as a unique virus on a long branch originating close to the trunk of the trees. Text states N, P, M, and F trees have FdIPV branching from the trunk of the tree, with no affinity for any known genus. Trees of HN and L proteins place FdIPV basal to the respirovirus branch, but close to the trunk of the trees. Figure shows N and L trees as representatives of these patterns. Suggests new genus named "*Ferlavirus*", with FdIPV as type species.

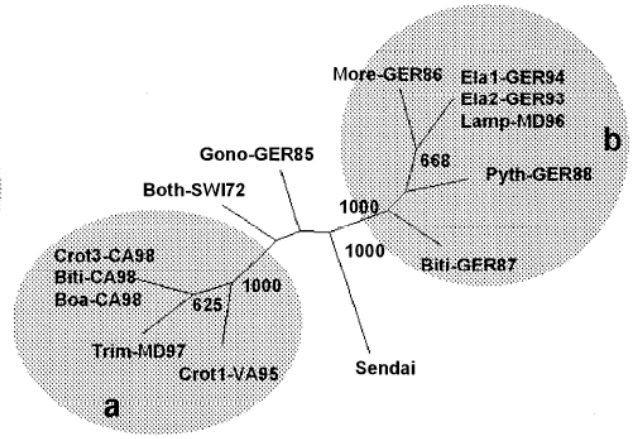


Phylogenetic trees for all common paramyxovirus proteins, showing separation of FdIPV from all established paramyxovirus genera and viruses. The HN and L trees were presented as Figure 4 in Kurath et al., 2004.

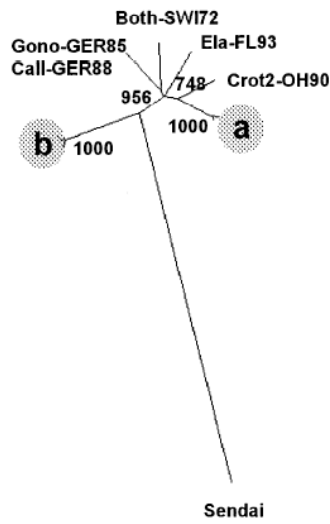
A) partial L gene



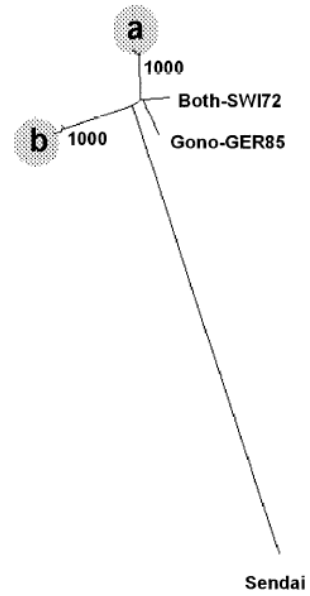
B) partial HN gene



C)



D)



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Ahne 1999 Figure 4, showing clusters A and B and several intermediate viruses including FdIPV: **NOTE that FdIPV is referred to in these trees by its isolate synonym "BothSWI72",** for isolation from a Bothrops snake in Switzerland in 1972. Partial L gene sequences are in A) parsimony and C) Neighbor-joining, and partial HN gene sequences are in B) parsimony and D) Neighbor joining. Note especially panels C and D, with branch lengths scaled to indicate accurate genetic distances. This is what suggests clusters A and B as groups of isolates that may be separate species, but alternatively they could be strains of FdIPV. Their placement requires additional sequence information.

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