

Evidence for multiple recent species jumps among the ranaviruses (family *Iridoviridae*).

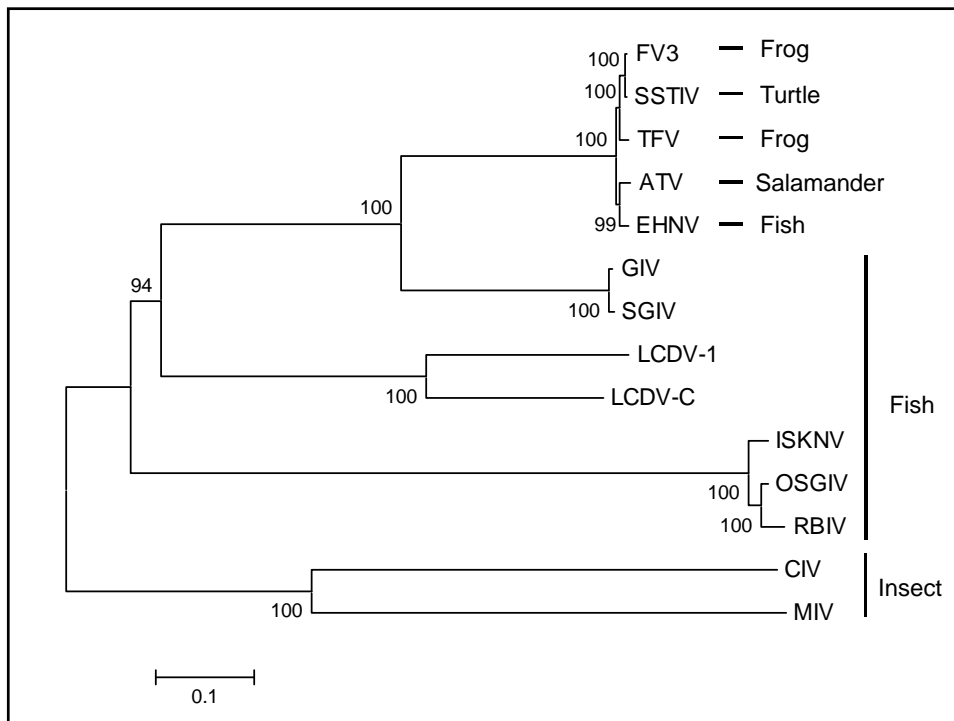


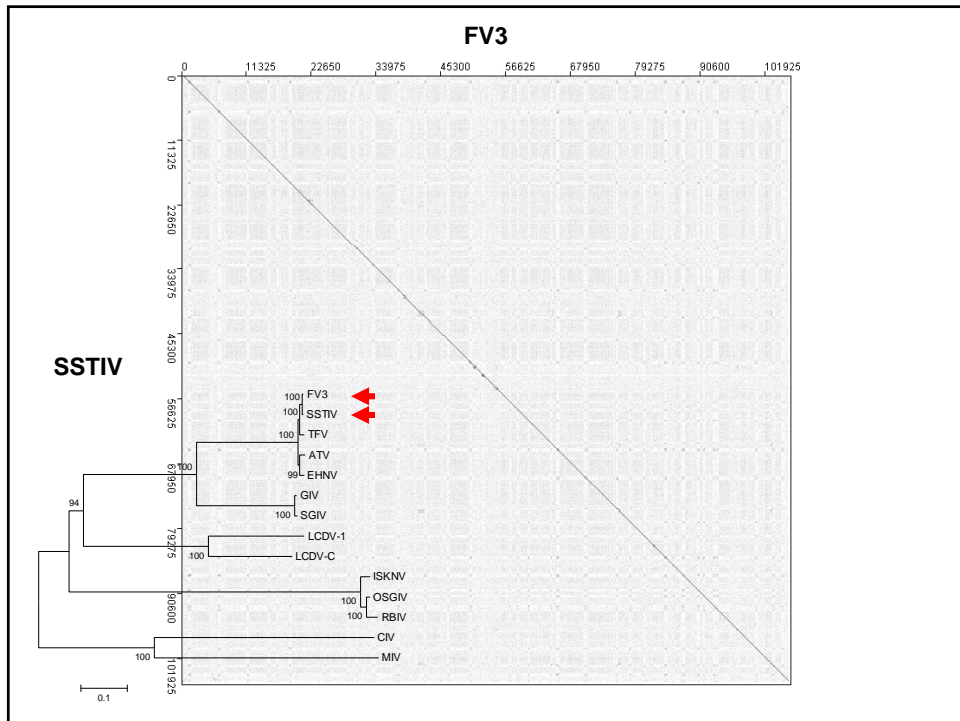
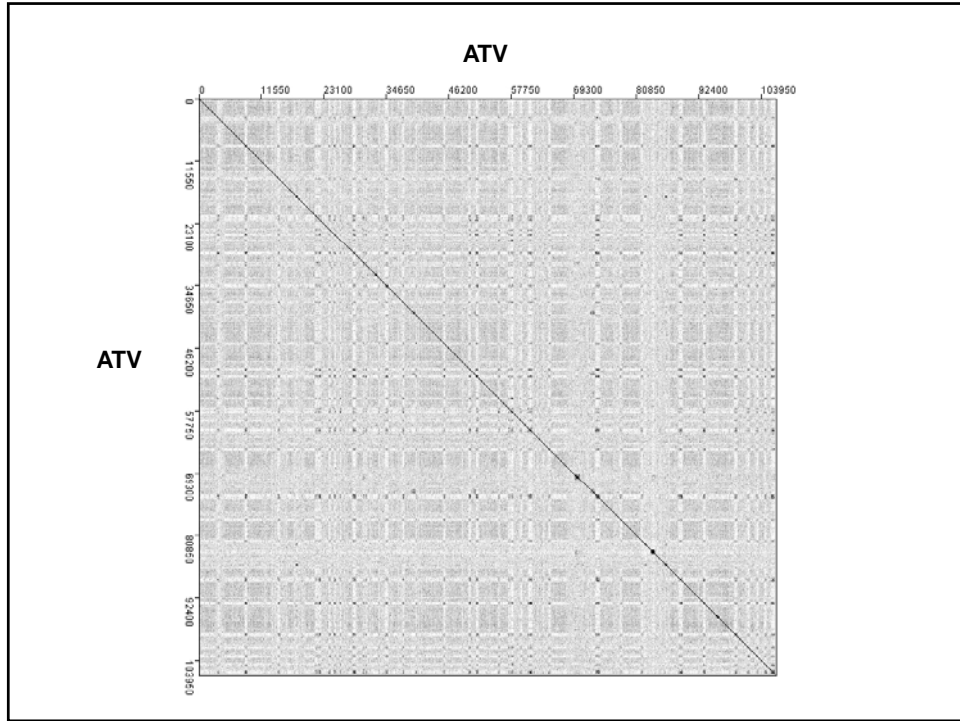
Completely Sequenced Iridoviruses

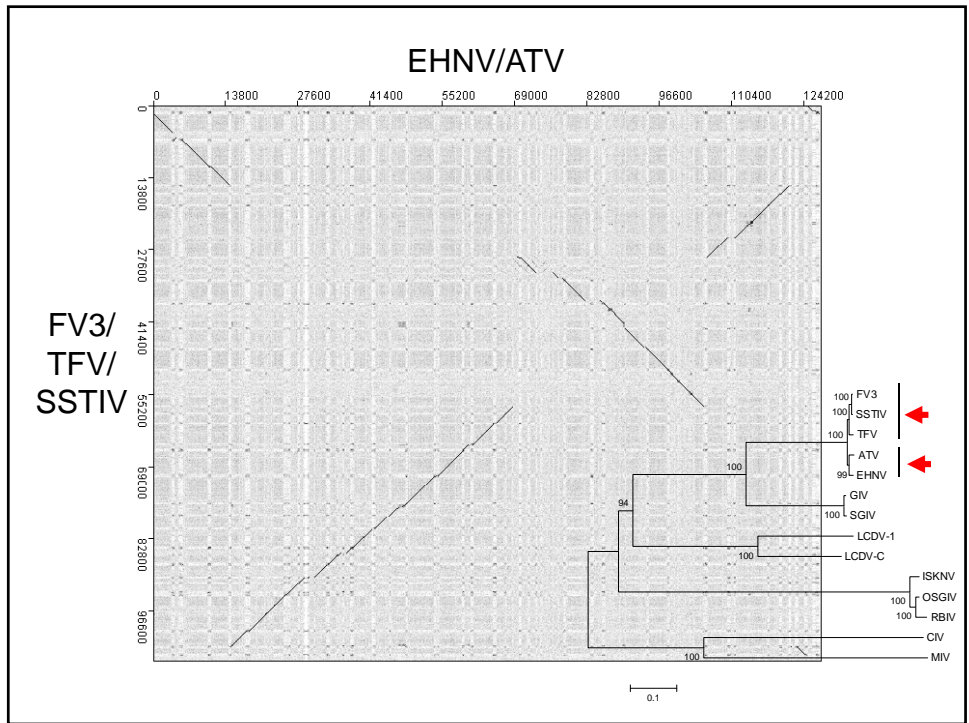
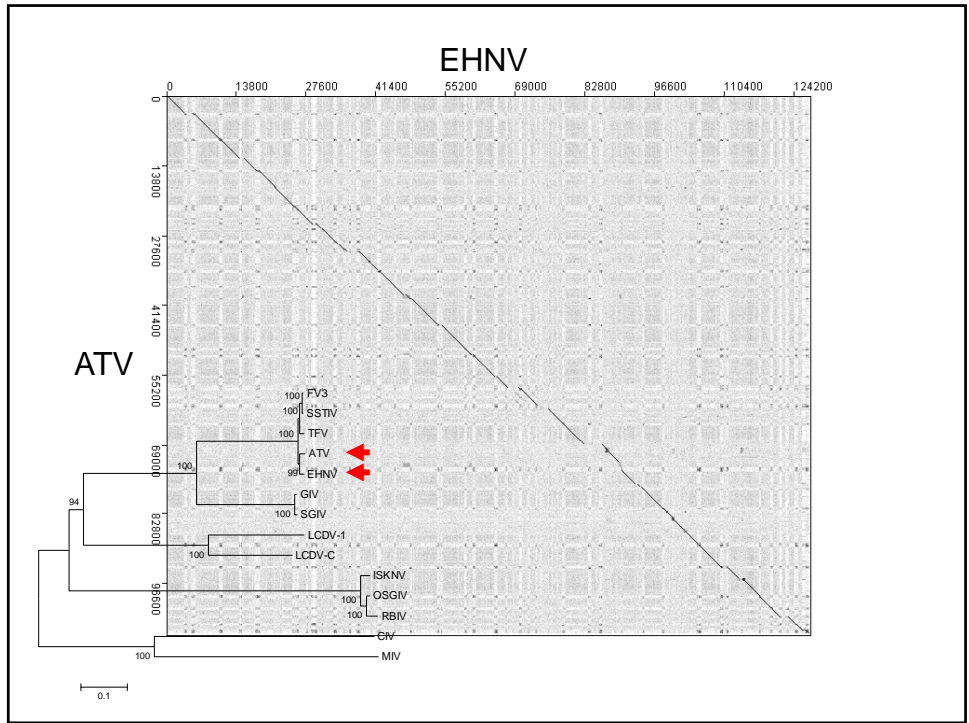
Genus	Virus	Known Host	Genome size (kb)	GC content (%)	Number of potential genes	Accession #
<i>Ranavirus</i>	ATV	salamander	106,332	54	92	AY150217
	EHNV	fish	127,011	54	100	FJ433873
	FV3	frog	105,903	55	97	AY548484
	SSTIV	turtle	105,890	55	105	EU6277010
	TFV	frog	105,057	55	103	AF389451
	SGIV	fish	140,131	48	139	AY521625
	GIV	fish	139,793	49	139	AY666015
<i>Megalocytivirus</i>	ISKNV	fish	111,362	55	117	AF371960
	OSGIV	fish	112,636	54	116	AY894343
	RBIV	fish	112,080	53	116	AY532606
	TRBIV	Fish	110,104	55	115	GQ273492
<i>Lymphocystivirus</i>	LCDV-1	fish	102,653	29	108	L63545
	LCDV-C	fish	186,247	27	178	AY380826
<i>Iridovirus</i>	IIV-6 (CIV)	insect	212,482	29	211	AF303741
	IIV-9	Insect	205,791	31	191	
<i>Chloriiridovirus</i>	IIV-3 (MIV)	insect	190,132	48	126	DQ643392

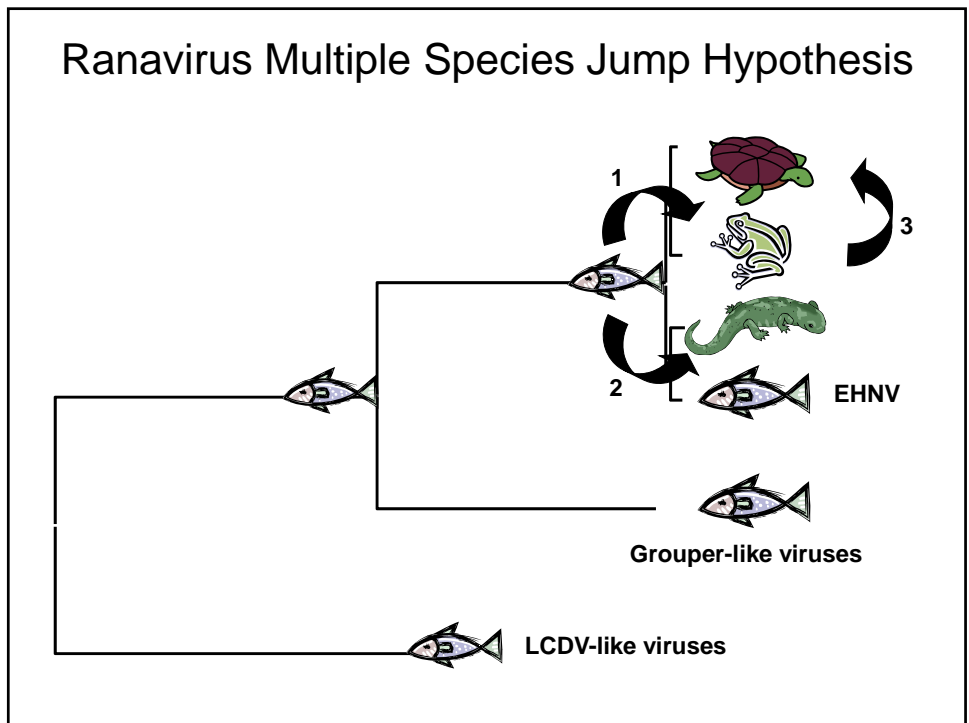
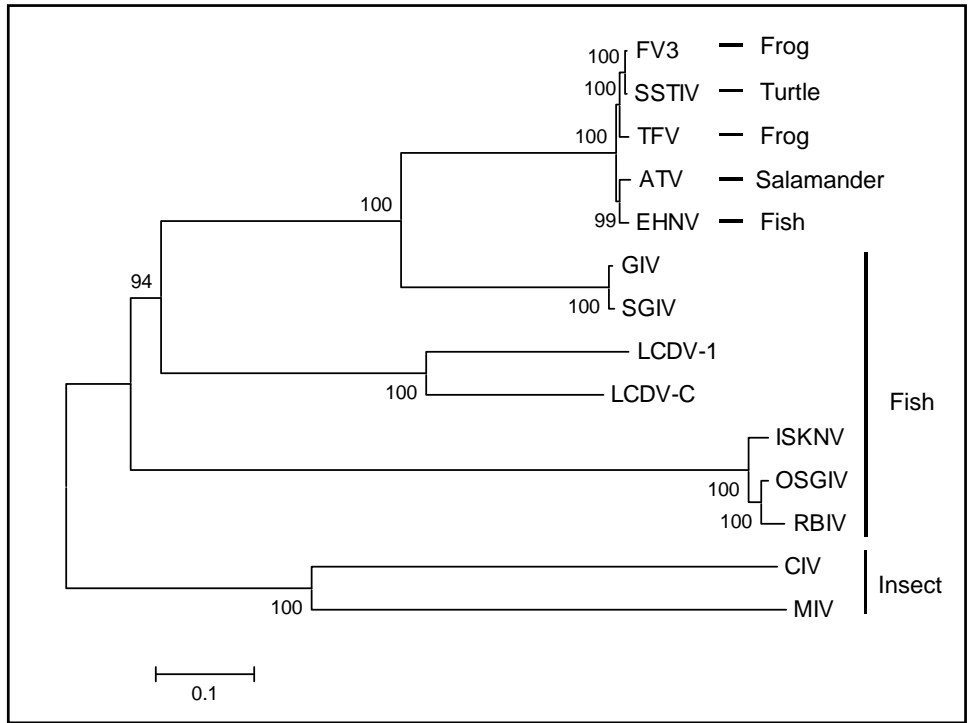
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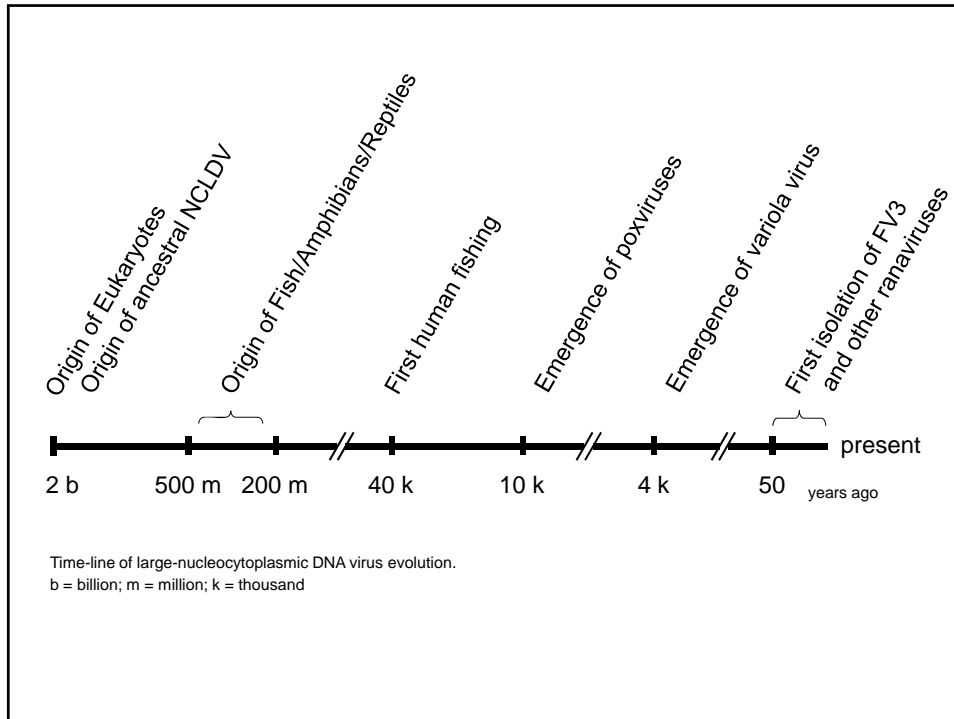




- Ranavirus genomic sequence comparisons
 - recent multiple species jumps
- World-wide translocation of animals may facilitate the continual spread of these infectious agents

Where do we go from here?

- When, in evolutionary history, have the observed species jumps occurred?



Where do we go from here?

- When, in evolutionary history, have the observed species jumps occurred?
 - genomic sequencing of ranavirus isolates
 - molecular clock of ranavirus evolution
 - comparative genomics
 - phylogenetics
- What molecular events facilitate species jumps?
 - host range/pathogenesis genes
 - changes in host biology

Acknowledgements

- Bert Jacobs
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