

RANAVIRUS TAXONOMY AND PHYLODYNAMICS

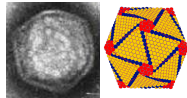
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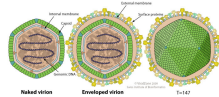
Talk Objectives

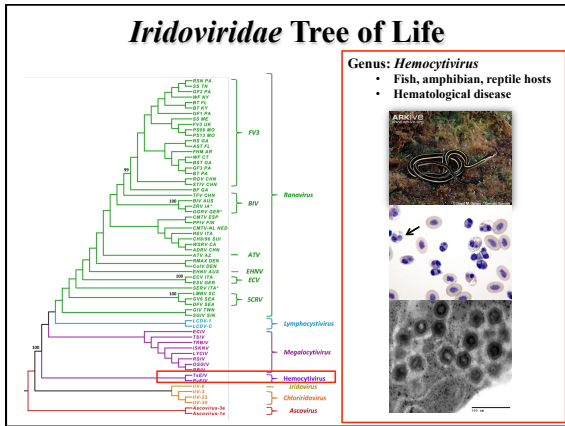
- Introduction to the family *Iridoviridae*
 - Taxonomy and basic biology
- Introduction to the genus *Ranavirus*
 - Taxonomy and basic biology
- Phylogenomic patterns
 - Gene trees
 - Genome organization
- Phylodynamic modeling
 - Expanding geographic and host ranges
 - Recombination

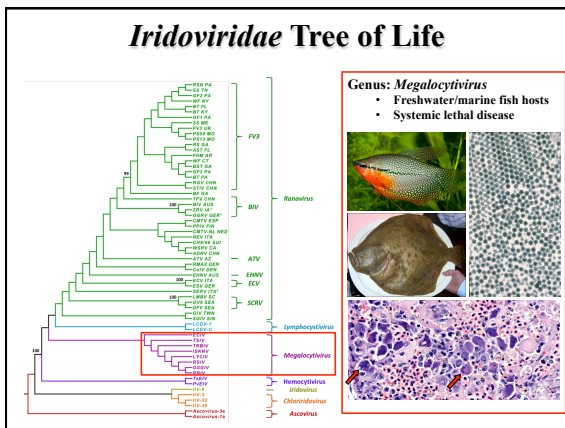


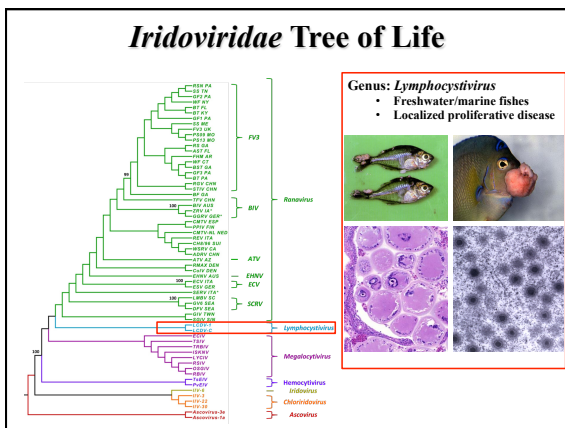
Family *Iridoviridae* Taxonomy

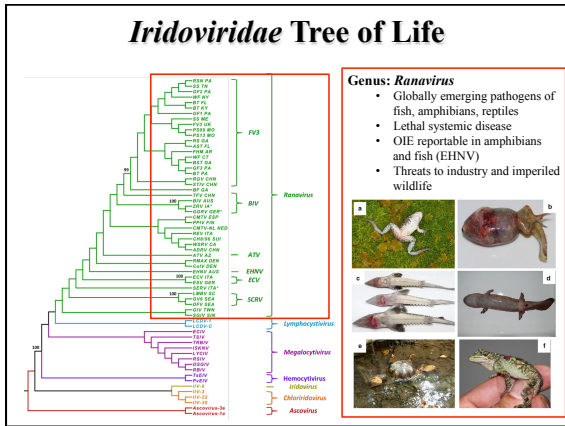
- Diverse group of Nucleocytoplasmic Large dsDNA Viruses (NCLDV)
- Virion: enveloped icosahedral capsid (120-350 nm)
- Taxonomy
 - Genus *Iridovirus* (arthropod hosts)
 - Genus *Chloriridovirus* (arthropod hosts)
 - Genus *Lymphocystivirus* (fish hosts)
 - Genus *Megalocytivirus* (fish hosts)
 - Genus *Ranavirus* (fish, amphibian, & reptilian hosts)
 - FV3, BIV, EHNV, ATV, ECV, SCRIV
 - Unassigned members: CMTV, REV, ADRV, CoIV/RMAX, SERV, SGIV/GIV
 - Unassigned members: EIVs (fish, amphibian, & reptilian hosts)

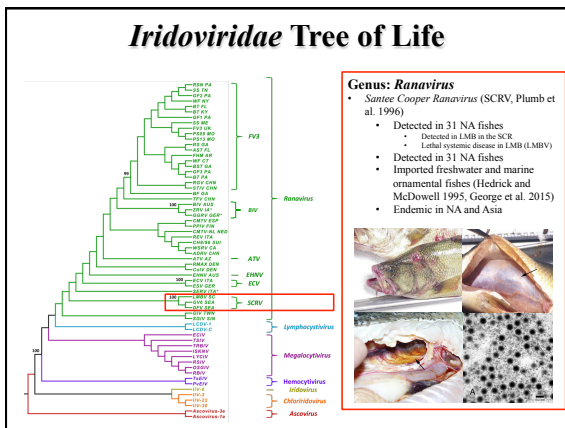


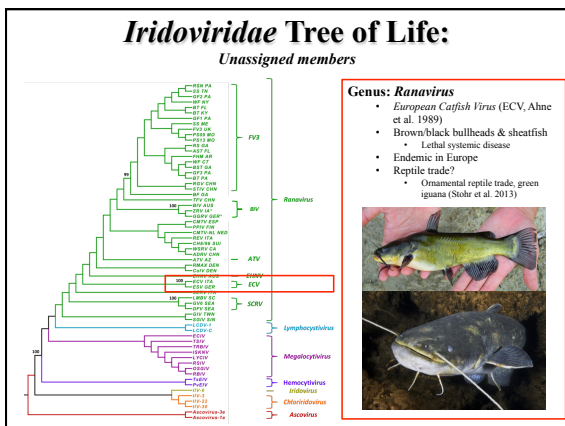


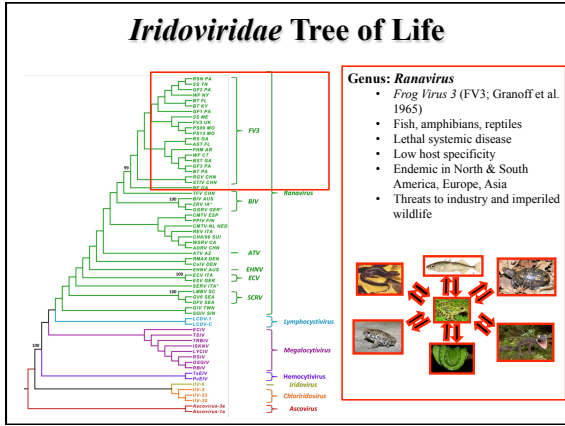


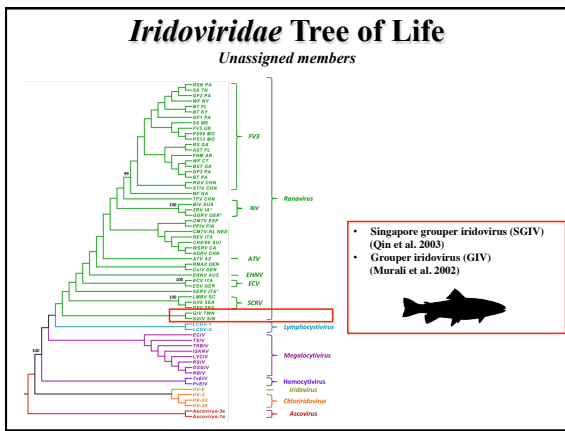


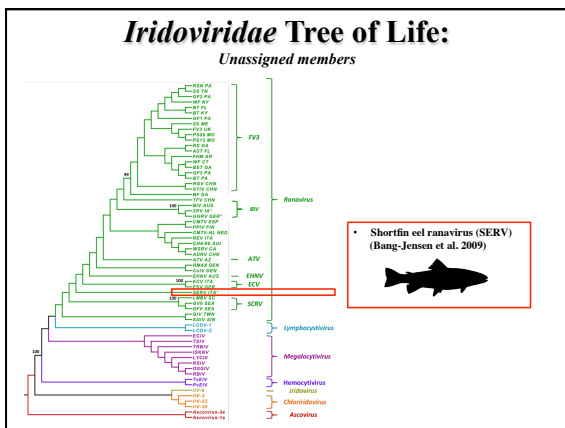


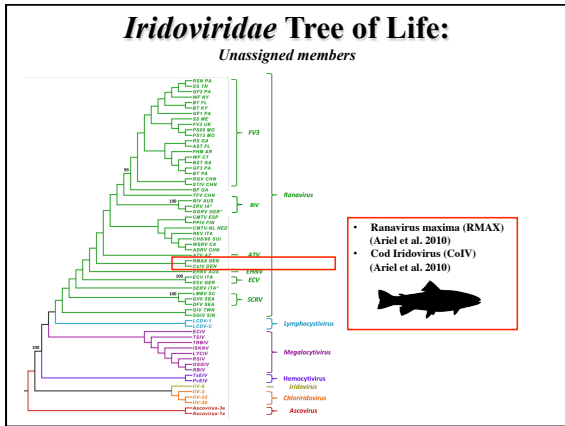


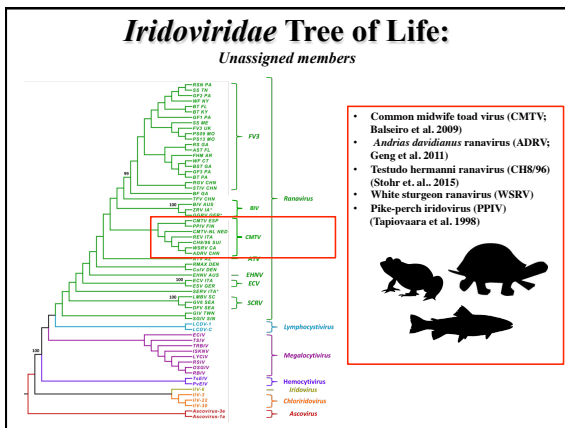


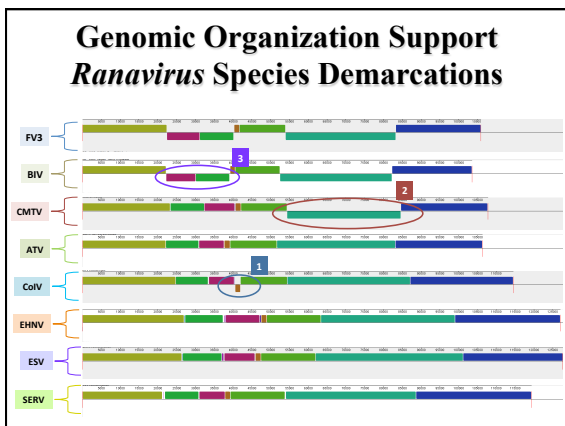


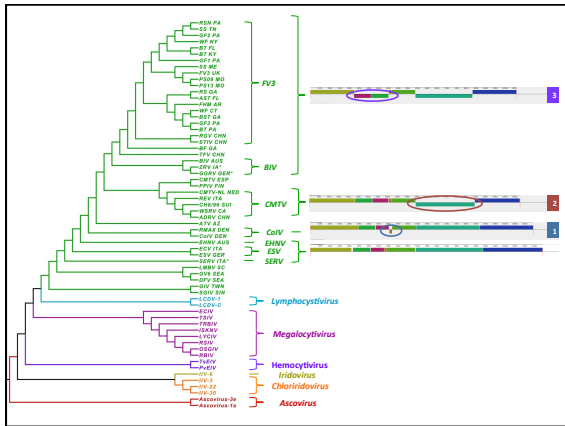


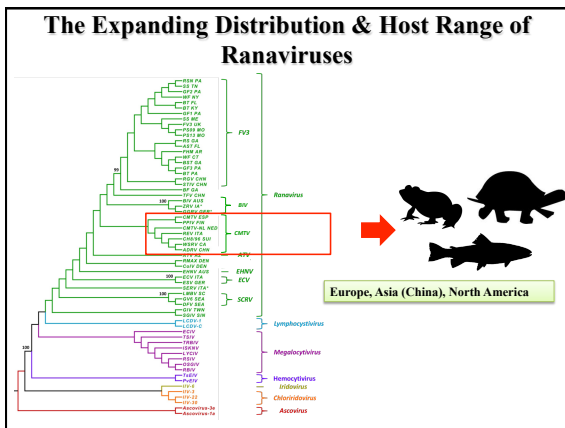


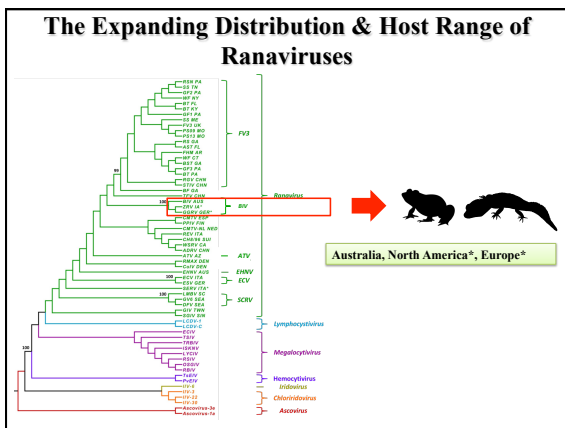


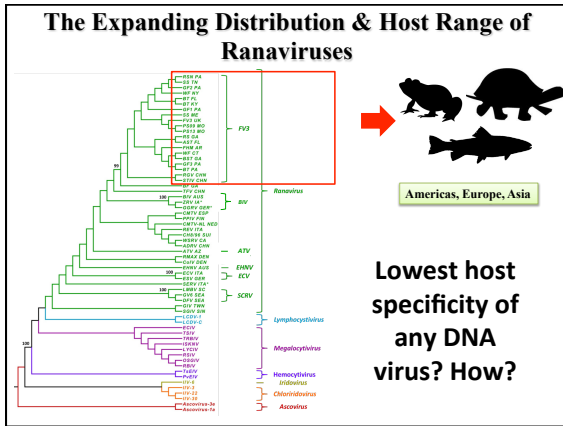












Ranavirus Host Range Evolution

- Could recombination be a driver of host range evolution and virulence? Virus outpaces host through recombination...
- Two bullfrog ranavirus isolates from the same aqua/ ranaculture facility sequenced
- Genomic sequencing reveals 1st isolate is CMTV, 2nd is FV3
- Recombination analyses (RdRP4.46b) reveals significant recombination between the FV3 and CMTV strains!

A genomic map showing the RdRP4.46b region of Ranaviruses. It illustrates recombination between CMTV and FV3 strains, with segments from both parents present in the offspring.

Conclusions

- NGS & global collaboration facilitated sequencing of 33 iridoviruses < 1 yr
- ML analysis (19 iridovirus core genes) produced the most comprehensive *Iridoviridae* tree to date
- Phylogenomic analysis supports the creation of a novel genus for EIVs (Hemocytivirus)
- Phylogenomic analysis supports the current *Ranavirus* species demarcations and the potential creation of new species (CMTV, SGIV/GIV, CoIV/RMAX, SERV)
- The geographic and host ranges of certain ranaviruses appears to be broader than previously realized (FV3, BIV, CMTV)
- Preliminary phylogeographic analysis suggests that the unregulated international movement of live animals (bullfrogs) and their products may explain the global distribution of FV3
- Recombination among ranaviruses may be a driver of host range evolution and virulence!

Acknowledgements

- University of Florida**
- Dr. James Welleslan
 - Dr. Natalie Steckler
 - Dr. Kuttichantran Subramaniam
 - Dr. Marco Salemi
 - Dr. Taj Azarian
 - Siara Claytor
 - Linda Archer
 - Patrick Thompson

- Istituto Zooprofilattico delle Venezie, Italy**
- Dr. Anna Toffan

- Finnish Food Safety Authority Evira**
- Dr. Riikka Holopainen

- Technical University of Denmark**
- Dr. Niels Jorgen Olesen

- Washington State University**
- Dr. Jesse Brunner

- University of Tennessee, Knoxville**
- Dr. Matthew Gray
 - Dr. Debra Miller

- California State University**
- Dr. James Jancovich

- Kasetsart University, Thailand**
- Dr. Jaree Polchana
 - Dr. Somkiat Kanchanakhan

- James Cook University, Australia**
- Dr. Ellen Ariel

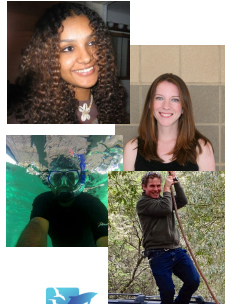
- University of Sydney, Australia**
- Dr. Richard Whittington
 - Dr. Paul Hick



Acknowledgements

Siara Claytor, MS

- MS student
- Viral isolation, genome assembly, gene extraction



Natalie Steckler, DVM, MS

- PhD candidate
- Viral isolation, gene extraction, tree generation

Kutti Subramaniam, MS, PhD

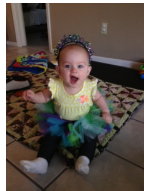
- Postdoctoral associate
- Genome assembly, gene extraction

Patrick Thompson, BS

- Biological scientist
- Viral isolation, next generation sequencing



Thanks for Your Attention! Questions?



A Special Thanks to the GRC!

Questions?

