A Novel Pegivirus in Indian River Bottlenose Dolphin

Talk Outline

- Indian River Lagoon (IRL) – Overview
- Introduction to the HERA project
- Discovery of Novel Pegivirus in Bottlenose Dolphin
- Genetic Characterization of Bottlenose Dolphin Pegivirus
- Future Directions
The Indian River Lagoon (IRL)

- An estuary of National Significance
- 40% of Florida’s East Coast
- Most Bio Diverse Estuary in U.S. (~ 4,000 spp.)
- Commercial & recreational activities support ~ 19,000 jobs & generate > $250 m in annual income

Image credit: St. Johns River Water Management District & UCF
IRL – Agriculture Based

- Rapid Development and Population Increase:
  - Influx of pollutants from water runoff
  - Increasing levels of copper and mercury
- Key Concerns - loss of seagrass meadows, oyster beds, mangrove habitat, toxic algal bloom, water quality, and fish kills

Image credit: Indian Riverkeeper (©Jacqui Thurlow-Lippisch)

Image credit: TCPALM
The Dolphin Health and Environmental Risk Assessment Program (HERA)

Collaborative, multi-disciplinary and integrated research program designed to access environmental and anthropogenic stressors, and determine the health and long-term viability of Atlantic Bottlenose dolphin populations
HERA Research Projects

- Surveillance for Emerging Infectious Diseases
- Assess Immune Status of IRL Dolphins
- Antibiotic Resistance Patterns and Exposure Sources
- Molecular Genetic Studies / Disease
- Health Effects of Mercury, PCB, and Organochlorine Exposure
- *2012 - 2013 UF WAVDL joins HERA!*
July 2012 IRL Sampling

- 12 Dolphins Sampled
  - Blood (buffy)
  - Fecal
  - Blowhole

- UF WAVDL Virus Discovery
  - Samples processed for next generation sequencing (NGS)
  - Samples frozen back for virus isolation
Discovery of a Novel *Pegivirus* in Bottlenose Dolphin

- RNA from serum, fecal, and blowhole were extracted using Qiagen kit
- A cDNA library was generated & sequenced using a v3 chemistry 600-cycle kit on a MiSeq platform (Illumina)
- *De novo* assembly was performed in CLC Genomics, SPAdes, & Velvet
- Blastx searches of the assembled data retrieved near complete genome of a novel *Pegivirus* (Family *Flaviviridae*) from serum samples
Family *Flaviviridae*

*Flavivirus* infects mammals and birds, for example, *Bovine Viral Diarrhea* infects pigs and ruminants, while *Hepacivirus* infects horses, rodents, bats, cows, and primates, causing progressive liver disease in humans, such as *hepatitis C virus*.

*Pestivirus* infects pigs and ruminants, as indicated by *Bovine Viral Diarrhea*.

*Arthropod borne viruses* infecting mammals and birds include *tick-borne*, *Mammalian*, and *Modoc* vectors.

*Unknown vector* is also depicted.

*Image source: https://talk.ictvonline.org*
Genus *Pegivirus*

A. New World monkeys & African bats

B. Asian & African bats

C. Old World primates

D. Pigs

E. Horses

F. Old & New World bats

G. Old & New World bats

H. Primates

J. Rodents

Legend:
- ● Human
- ○ Primate
- ■ Horse (dog)
- □ Pig
- ▲ Bat
- △ Rodent

Distance scale: 0.2
Dolphin pegivirus (DPgV)

- The genome is 9,649 bp and encode a polyprotein which is cleaved by viral and cellular proteases into structural and non structural proteins.
Serological Evidence of Flavivirus in IRL Dolphin

- Sera from 122 IRL dolphins were collected from 2003-2007
- Analyzed for antibodies to several bacterial and viral pathogens
- Seropositive to West Nile virus (flavivirus)
Phylogenetic Analysis

Maximum Likelihood analysis based on the conserved domains in IQ-TREE
Phenetic Analysis

- Comparison of conserved domains of DPgV to other pegiviruses showed sequence identity ranged from 40.6 – 54.6%

- The ICTV suggests a species demarcation threshold of <69%

- DPgV is the first pegivirus described from marine mammal & propose to be accepted as Pegivirus L within the genus Pegivirus
Future Directions

- Complete the genome sequence by RACE

- Development & validation of molecular tools
  - RT-qPCR
  - *In situ* hybridization
THANK YOU FOR THE ATTENTION!

ANY QUESTIONS?