

Eastern indigo snake bacterial disease



Project Description:

Florida wildlife officials have recently recorded an increased mortality in populations of the native, endangered Eastern indigo snake (*Drymarchon couperi*). Veterinarians have discovered an unusual level of bacteremia in many of the deceased snakes, suggesting a bacterial pathogen. Initial work has also suggested that the bacteria may be a spotted-fever group rickettsia, similar to *Rickettsia raoultii*. Oddly these Rickettsia are only known to be transmitted by ticks of the genus *Amblyomma* in snakes from Thailand ([read more here](#)). You have been awarded a grant to characterize this potential outbreak in hopes of mitigating future loss of this endangered and iconic reptile species of Florida.

Additional Facts:

- 1) Florida is famous for its invasive populations of reptiles due to the import of wild animals from overseas for the pet trade
- 2) Rickettsia are obligate, intracellular pathogens that prefer endothelial cells of blood vessels (in essence, difficult to culture, only cultured in host cells)
- 3) Florida has two native *Amblyomma* tick species, *A. americanum* and *A. maculatum*
- 4) The only snake genomes available are distantly related to the indigo snake, but one of them, the Burmese python, is also invasive in Florida.
- 5) Numerous Rickettsia genomes from many species/strains have already been sequenced.
- 6) Florida officials can provide you with any and all samples you need.

Goals:

Using **genomic tools only**, we would like to characterize the pathogen, the vector, and its origin. Since the ultimate theme of this exercise is to design 'Best Practices', carefully consider the following:

- Which samples will be collected and how will they be documented?
- Which genomic methods/tools will be used and why were they chosen?
- What other sources of data/information are needed (e.g., GenBank)?
- How will the data and results be archived and/or disseminated?
- How should the findings be validated?

Retroviral resistance in a re-discovered tarsier species



Project Description:

A formerly 'extinct' species of tarsier (Pygmy tarsier) has been re-discovered in the rain forests of Sulawesi (This is actually true). Unlike other primates, it is completely immune to a retrovirus that is causing a pandemic among other tarsier species in Indonesia. Local and regional biologists and educators are hoping to highlight this iconic pygmy tarsier to help in conservation management programs, global awareness, and demonstrate how comparative medicine and genomics can find cures for retroviral diseases.

Additional Facts:

- 1) The biology of the retrovirus in other primates is well known including host receptor usage and 50 host genes that are hijacked by the retrovirus during its life cycle.
- 2) The retrovirus has been sequenced in entirety and compiled into a database of over 100 distinct strains.
- 3) Let's suppose that there are 3 genera, and 11 species of tarsiers (actually true), and it appears that the pygmy tarsier might have 3 unique subspecies that are geographically distributed. So far, we have only determined that one subspecies is completely resistant to disease.
- 4) You are an expert in primate evolution and speciation, somewhat familiar with retroviruses, but rather ignorant about host-virus interactions on the genomic level.
- 5) Only 1 tarsier genome sequence exists – from a different genus

Goals:

Using **genomic tools only**, we would like to characterize the disease resistance of the pygmy tarsier. Since the ultimate theme of this exercise is to design 'Best Practices', carefully consider the following:

- Which samples will be collected and how will they be documented?
- Which genomic methods/tools will be used and why were they chosen?
- What other sources of data/information are needed (e.g., GenBank)?
- How will the data and results be archived and/or disseminated?
- How should the findings be validated?

Viral biocontrol of an invasive rat species



Project Description:

You have been awarded a large grant by the nation of Islandia to combat a serious problem they are having with a population of non-native rats (a species in the genus *Rattus*). Since being introduced to Islandia, these rats have negatively impacted a variety of native animal populations and are eating all the crops. Despite the checkered history of similar efforts, Islandia wants you to develop a viral biocontrol strategy.

Your resulting strategy should have the following characteristics:

- 1) be specific to the targeted rats
- 2) cause significant mortality in the rats
- 3) be likely to spread through the population (have a high R_0 value).

Additional Facts:

- 1) You have evaluated several known candidate viruses, but these didn't satisfy the above criteria, so you will have to discover and evaluate a new virus for this purpose.
- 2) You have unlimited funds for sequencing

Goals:

Using **genomic tools only**, we would like to characterize a biocontrol strategy/pathogen. Since the ultimate theme of this exercise is to design 'Best Practices', carefully consider the following:

- Which samples will be collected and how will they be documented?
- Which genomic methods/tools will be used and why were they chosen?
- What other sources of data/information are needed (e.g., GenBank)?
- How will the data and results be archived and/or disseminated?
- How should the findings be validated?

Permafrost pathogen outbreak!



Project Description:

You are part of an international response team that is investigating a fatal disease cluster in both wild and domestic ungulates in a remote corner of Siberia. The disease seems to have an infectious origin, and regional public health experts suspect it was caused by a pathogen contained in a reindeer carcass frozen for thousands of years in permafrost that is now melting because of climate change (Note that this is a not implausible scenario: [Anthrax Outbreak In Russia Thought To Be Result Of Thawing Permafrost](#)). Your team's task is to investigate this cluster. You will use an NGS-based approach to attempt to identify the possible pathogen.

Additional Facts:

1. The index case is believed to be from a feral domestic goat that had fed near the carcass.
2. Unfortunately, all verified cases have died, and there is no access to samples from them.
3. The only samples you have are from the partially thawed reindeer carcass.
4. You unlimited access to all types of DNA sequencing.

Goals:

Using **genomic tools only**, we would like to characterize the potential pathogen. Since the ultimate theme of this exercise is to design 'Best Practices', carefully consider the following:

- Which samples will be collected and how will they be documented?
- Which genomic methods/tools will be used and why were they chosen?
- What other sources of data/information are needed (e.g., GenBank)?
- How will the data and results be archived and/or disseminated?
- How should the findings be validated?