Ranaviruses: Prevalence, effect, and transmission among native amphibians in Vermont

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**Title**:

**Summary/Specific Aims?:**

**Intellectual Merit (knowledge gaps)**:

**Introduction**:

**(3-4) Objectives (Questions?)/Hypotheses/Background/Approach: Think of different chapters as separate papers; could change objectives to questions**

**Objective I:** Conduct a field survey to elucidate the prevalence and viral load of *Ranavirus* in native amphibian communities of Vermont to a) determine if any of the pathogens are present and affecting Vermont amphibians and b) determine the variety of strains present in communities (phylogenetics); modeling (predictive and epidemiological) determine which factors influence presence absence

Ranavirus book pg226 [MODELING]:

“One strategy would be to create several competing models and test them to data on dynamics in natural populations or in mesocosm studies to identify the most important mechanisms for transmission”

“Other model expansions could be particularly useful for predicting ranavirus dynamics in natural populations; studies could serve as a starting point for determining transmission probabilities in aquatic communities with multiple species”

**Objective II** experiment (evolution of virulence?) - genomics

**Objective III** population genetics – gene flow (migration) – landscape genetics (not disease related?)

Vertical transmission hypothesized: a study that controls for in vitro contamination has not been performed. (2009 “Ecology and pathology of amphibian ranaviruses” Gray, Miller, Hoverman)

Q1: Are ranaviruses present in native Vermont amphibian communities, and if so, what is the diversity of strains and how virulent are they? (presence with qPCR; diversity with qPCR and phylogenetics [invasion history?]; viral load with qPCR to determine how virulent]

Q2: Which factors are influencing presence, virulence, and transmission of the disease? (predictive modeling with other data points in specific time frame to determine presence factors [possibly give info on virulence and transmission]; epidemiological models to predict natural ranavirus dynamics [transmission/virulence/host or reservoir species/variation])

Q3: Does the host genetic structure influence the effects of the pathogen on the host? (compare population genetic structure of sites that are present vs absent; conduct experiment to obtain genomic data)

Q4: Are leeches potential vectors of the pathogens? (test collected leeches for disease using qPCR; if found, conduct experiment)

**Hypothesis I:** There is

**Hypothesis II:** There is

**Hypothesis III:** There is

**Background**:

**Approach**:

**Broader Impacts**:

**References**: