A Bayesian approach to genetic data (PCR) to better understand fish disease dynamics

Nikolaos Fytilis, Donna M. Rizzo, Lori Stevens, Ryan Lamb, Billie Kerans

Environmental managers and ecologists are increasingly required to forecast long-term effects, resilience, and vulnerability of biophysical systems due to the presence of a contaminant or disease. *Myxobolus cerebralis* is a fish parasite that causes whirling disease by damaging neurological functions, a major detriment to salmonid populations in the western USA. Since the 1950s, when this disease was introduced to North America, there has been marked spatial variation in its effects on salmonid populations. The worm *T. tubifex*- the intermediate host of this parasite- lives in diverse assemblages. *T. tubifex* genetic lineages vary in susceptibility from highly competent (lineage III *T. tubifex*) to nearly incompetent (lineage I *T. tubifex*), and often co-occur with non-host tubificids (i.e., *Rhyacodrilus spp.*). A problem in understanding whirling disease epidemiology is that Rhy and Tt can only be distinguished based on morphology as sexually mature adults, and only DNA sequence data can distinguish *T. tubifex* lineage III and I.

To study spatial variation in whirling disease, we developed two multiplex molecular genetic probe-based polymerase chain reaction (PCR) assays. Assays were verified by comparison with sexually mature adults and DNA sequence of immature collected from eight sites along the Madison River, MT that vary in whirling disease risk. To test the hypothesis that worm assemblages influence whirling disease risk, we show that a Bayesian approach can improve identification of the worm taxa using PCR data. Bayesian analysis of the PCR data helps us estimate the worm community composition and reveal relationships between biodiversity of host communities and host-parasite dynamics. The ability to characterize areas of high whirling disease risk is essential for improving our understanding of the dynamics of *M. cerebralis*. Future work includes development of a new complex systems tool capable of assimilating DNA sequence and biogeochemical data using artificial neural networks and Bayesian analysis.