Wednesday September 5th – Tilly / Tupper
Aquatic Epidemiology 2
Moderator - Ian Gardner (Atlantic Veterinary College - UPEI)

1:45 PM	Aquatic Epidemiology 2	Gautam - A GIS-based Multi-Criteria Analysis Framework to Inform Risk-based Surveillance of Wild Aquatic Animals in Freshwater System
2:00 PM		Jung-Schroers – Epidemiological Study on the Occurrence and the Pathogenicity of the Carp Edema Virus (CEV) in Fish in Germany
2:15 PM		Laurin – Guidelines for Pooling Samples for use in Surveillance Testing of Infectious Diseases in Aquatic Animals
2:30 PM		**Lopez-Porras – A Molecular Survey of Bacterial Fish Pathogens in Nile Tilapia *Oreochromis niloticus* Hatcheries in Costa Rica**
2:45 PM		**Patanasatienkul – Mathematical Modeling to Optimize Mitigation Strategies against *Ciona intestinalis* in Mussel Production**

A GIS-Based Multi-Criteria Analysis Framework to Inform Risk-Based Surveillance of Wild Aquatic Animals in Freshwater System

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Surveillance is necessary to establish zones of disease presence and/or absence. Risk-based surveillance is a type of surveillance that helps in effective allocation of resources, and increases the probability of disease detection. This increased likelihood of detection is achieved by focusing surveillance effort on populations and areas at greater risk of disease introduction and establishment. The identification of high risk populations and areas can, however be a challenge, particularly in natural aquatic systems. Such challenges may include the distribution of susceptible host population(s) in an environment consisting of thousands of water bodies. To simplify this complexity, a multi-criteria analytical tool evaluating the likelihood of pathogen entry from an infected source population to a population of interest was developed using four possible pathways of pathogen transfer. These four pathways of pathogen transfer were: (i) hydrological connection, (ii) anthropogenic movement of live animals, (iii) anthropogenic movement of eggs and/or germplasm, and (iv) vectors and fomites. Each of these pathways received a likelihood score between 0 and 1 depending on specific criteria. The relative importance of each of the pathways was also evaluated by weighting them. The weights were established by expert consultation. The population of interest was defined as any secondary watershed that did not have a known health status. The health status of the source population was defined as either infection free (0), unknown (0.5), suspect infected (0.75) or confirmed infected (1). Using the appropriate combination of the relative weight and likelihood score of each pathway, and the source population health status, pathway specific likelihood scores were calculated for all secondary watersheds. A total likelihood score of pathogen entry was then determined by adding the likelihood scores of all the pathways. Using this, the likelihood of exposure and potential infection was determined by considering the distribution of susceptible species and environmental conditions. The likelihood score for entry, exposure and infection were used to risk-categorize secondary watersheds in Canada and represented visually as risk maps, using Geographic Information System (GIS).The GIS maps can be used to identify and spatially visualize high risk areas and can be used as decision support tools to determine sampling locations for designing risk-based surveillance in aquatic animals. This model is presented using Whirling Disease and spring viraemia of carp in Canadian waters as examples.

Conference Session Designation: (Aquatic Epidemiology)
Presentation Format: (Oral)

Epidemiological Study on The Occurrence and the Pathogenicity of the Carp Edema Virus (CEV) in Fish in Germany

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Koi sleepy disease (KSD) caused by infections with the carp edema virus (CEV) seems to pose a potential risk to carp aquaculture and koi trade. During the years 2015 and 2016 an epidemiological study on the occurrence of CEV in fish in Germany was performed. In total 421 gill samples were analyzed. Most of these samples were taken from common carp or koi carp, only a few samples were taken from additional fish species that were kept together with carp. In 194 samples CEV genome fragments were detected. Most detections, in total 179, were made in samples from koi carp (*Cyprinus carpio*), in 61 samples of common carp (*Cyprinus carpio*) CEV was detected and in 1-2 samples each of *Ctenopharyngodon idella*, *Esox lucius*, *Gymnocephalus cernua*, *Perca fluviatilis*, *Sander lucioperca* genome fragments of CEV were found in low amounts (1.10E+00 – 1.19E+03). Highest amounts of viral DNA were detected in samples of koi carp (1.00E+00 – 4.82E+06) and common carp (1.00E+00 – 4.03E+06). Sequencing of the DNA fragments revealed that there are at least two different genogroups of the virus are present and that almost all isolates detected in common carp are belonging to genogroup 1 whereas almost all isolates detected in koi carp are belonging to genogroup IIa.

Characteristic symptoms for an infection with CEV were enophthalmus, anorexia, gill necrosis, gill swelling and lethargic behavior. Mostly in spring, between May and July, CEV was detected. In koi carp disease outbreaks due to CEV were mostly seen when the water temperature was between 17-18°C, whereas in common carp at water temperatures between 9-13°C CEV was detected most frequently.

In 46.66% of samples taken from clinically healthy koi or carp from retailers, CEV was detected. Taken all samples from clinically healthy koi and carp, CEV could also be detected, but only in 26.32% of all examined fish. Therefore purchasing new fish from retailers might be one risk factor for the introduction of CEV in a pond. In common carp more frequently diseases signs and mortalities were recorded compared to koi carp. The probability of losses of more than 50% in a system was around 5 times higher in common carp aquaculture than in facilities for koi carp. Fish health services should therefore be aware of the presence of CEV which may result in high losses in carp aquaculture and testing of koi and carp for CEV should become part of fish disease surveillance programs of national and regional fish disease laboratories.

Conference Session Designation: (Aquatic Epidemiology)
Presentation Format: **(** Oral)

Guidelines for Pooling Samples for Use in Surveillance Testing of Infectious Diseases in Aquatic Animals

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Specimens from multiple animals may be pooled and tested to reduce costs of surveillance for infectious agents in aquatic animal populations. The primary advantage of pooling is to provide better population coverage when prevalence is low (<10%), increasing the likelihood of including at least one infected animal in a pooled sample. However, critical questions still need to be addressed relating to the effects of pooling on diagnostic sensitivity of a test used for a surveillance system supporting claims of disease freedom. Unfortunately, many of the pooling recommendations in the 2017 OIE Manual of Diagnostic Tests for Aquatic Animals are incomplete and not supported by peer-reviewed studies. No clear patterns were evident for pooling methods and characteristics from our systematic review of peer-reviewed aquatic diagnostic accuracy studies (DAS) using pooled animals (only 9 DAS with surveillance purposes out of 73 papers were identified). Therefore, the purpose of our study was to discuss pooling and interpretation of pooled sensitivity in DAS with surveillance purposes. A practical flowchart of pooling guidelines was developed that would be useful for peer-reviewed journals and for research institutions studying the comparative accuracy of individual and pooled tests for surveillance of infectious diseases of aquatic animals.

Conference Session Designation: **(** Diagnostics & Quality Assurance)
Presentation Format: (Oral)

A Molecular Survey of Bacterial Fish Pathogens in Nile Tilapia (*Oreochromis niloticus*) Hatcheries in Costa Rica

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Streptococcus spp., *Edwardsiella* spp. and *Francisella noatunensis* subsp. *orientalis* (Fno) are some of the most important fish pathogens affecting global tilapia (*Oreochromis* spp.) aquaculture. In Costa Rica, the aquaculture industry is dominated by fresh-water cultured Nile tilapia (*Oreochromis niloticus*), which is cultured in all seven provinces. At present, very little is known regarding the diversity of fish pathogens present in these systems and definitive diagnoses of agents associated with disease outbreaks are rare. To evaluate the prevalence of common pathogens within these systems, this study employed multiplex real-time PCR assays targeting several bacterial pathogens as a diagnostic and surveillance tool. In 2017, seven different tilapia hatcheries were visited, and 350 fingerlings were subjected to a complete necropsy and molecular diagnosis. Fish presenting with gross signs of disease were subjected to histological and microbiological analysis. For the first time, *Edwardsiella anguillarum* was recovered and molecularly confirmed from diseased tilapia in Costa Rica. Additionally, *Francisella noatunensis* subsp. *orientalis* was identified in a region of Costa Rica it had not been previously reported.

Conference Session Designation: **(** Aquatic Epidemiology)
Presentation Format: (Oral)
Student Presentation: (Yes)

Mathematical Modeling to Optimize Mitigation Strategies Against *Ciona intestinalis* in Mussel Production

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Over the past two decades, the Prince Edward Island (PEI) mussel industry has been challenged with the infestation of invasive tunicate species, which foul mussel socks and culture gear, causing significant economic losses to the industry due to added production costs of biofouling control. Field experiments to find suitable mitigation strategies require considerable time and are resource intensive. We applied a mathematical model to assess several control strategies against *Ciona intestinalis* populations in PEI. A temperature dependent compartmental model incorporating environmental carrying capacity was used to model the total abundance of *C. intestinalis*. A mitigation strategy was defined as a combination of timing and frequency of treatments. Various strategies were explored to obtain the combination that maximized the difference in predicted abundances between the untreated and the different mitigation strategies. Treatment frequency was allowed to vary between one to four times over a given production year. The model was assessed under baseline conditions, which mimicked water temperatures from Georgetown Harbour, PEI, in 2008, and under scenarios that reflected prolonged summer or warm spring temperatures. Furthermore, the sensitivity of the model to variations in presumed treatment efficacy was evaluated. The use of all four available treatments, starting around the first week of July and correctly timed thereafter, provided the most effective strategy, assuming the baseline temperature scenario. However, the effectiveness of this mitigation strategy depended on temperature conditions. The mathematical model developed in this study allows decision makers to optimize different strategies to control the abundance of *C. intestinalis* in mussel production areas under different environmental conditions. In addition, the modeling framework developed can be adapted to simulate similar ectoparasitic infestation in aquatic environments.

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