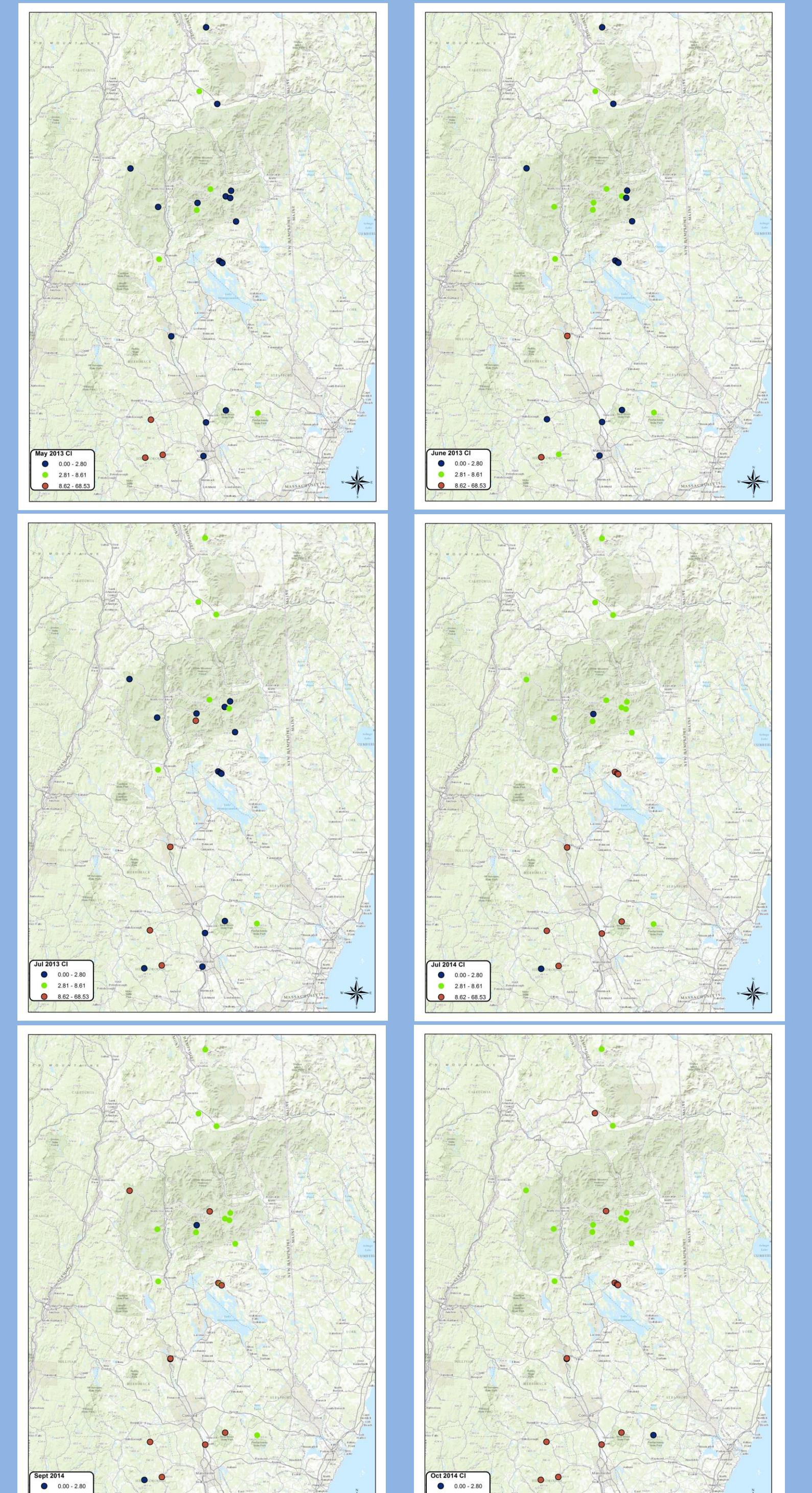
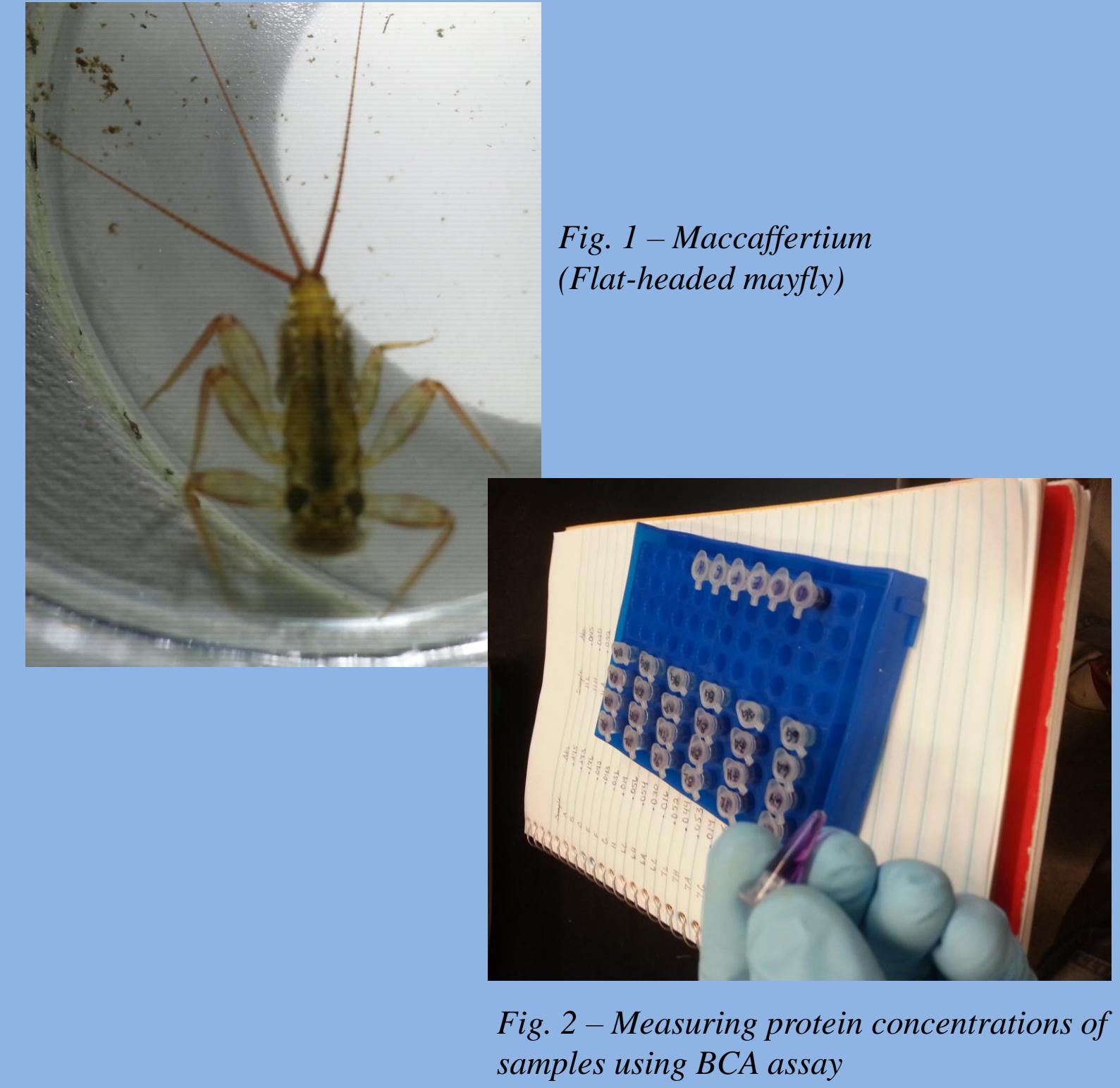


Stress Protein Expression: An Early Warning Sign of Freshwater Community Degradation via Road Salt Runoff in New Hampshire

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Background

The widespread application of chloride salt control products for winter travel safety has caused growing concerns over their impact to nearby aquatic ecosystems. In order to identify ecosystems affected by runoff of road salts, we hope to establish a simple, fast process for early identification of at-risk communities, essentially providing time for adjustment of road maintenance practices before the loss of sensitive species. We will be testing a new method of using mayflies as bioindicators of stream health with molecular techniques to examine the expression of heat shock proteins in mayfly nymphs.

- From 2008-2010, the number of documented streams in NH impacted by road salt runoff jumped from 19 to 40 (NH DES, 2014).
- Salinization of freshwaters has been observed to vastly alter benthic macroinvertebrate assemblages, particularly decreasing the variety of mayflies present (Doupe & Horwitz, 1995).
- Mayflies represent 25-50% of riffle taxa in some regions (Pond, 2010).
- Heat shock protein (HSP) are a class of molecular chaperones whose purpose is the protection and maintenance of other proteins in response to emergency stress (Lencioni et al. 2009; Hochachka & Somero, 2014)
- HSPs actively observed in natural populations in response to occasional stress exposures (Sørensen et al. 2003)

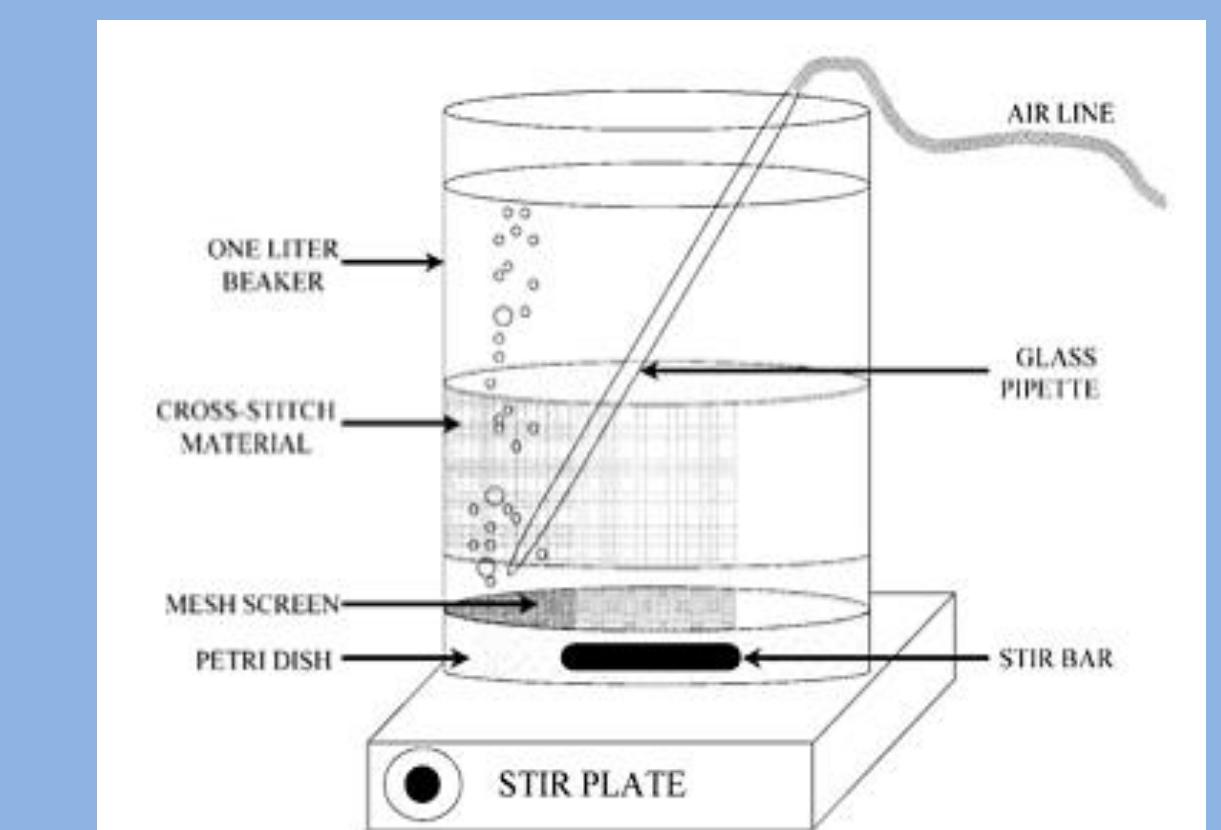
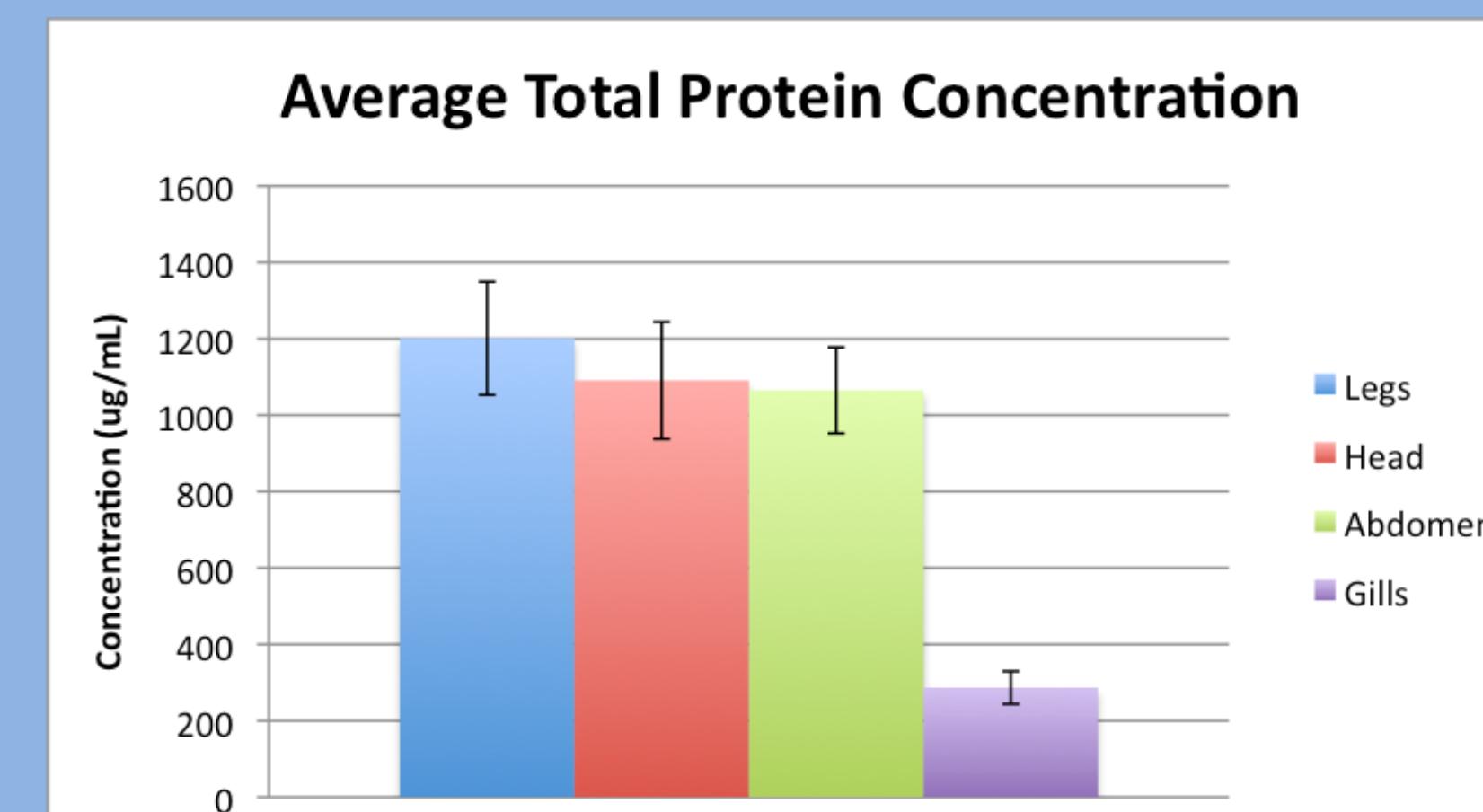
While a multitude of research has focused on the lethal dosages of NaCl exposure in mayfly nymphs, little has been accomplished in establishing sub-lethal indicators of osmotic stress, which may serve as a more sensitive and effective method for determining biotic responses to disturbance (Sørensen et al. 2003; Johnson et al. 2015).

Objectives

- Establish the location and degree of HSP expression throughout the mayfly morphology
- Develop standard curve describing the expression of HSP's in mayflies as a function of salt loading
- Examine levels of HSP expression in mayflies across a gradient of salt concentrations in NH streams

Current & Planned Research

- Analysis of HSP70 expression across mayfly morphology in *Maccaffertium* nymphs (Fig. 1)
 - Mayfly nymphs have been dissected into four body regions: Head, Gills, Legs and Abdomen.
 - Total protein content has been extracted using T-PER lysis buffer and quantified using a standard Bicinchoninic Acid Assay (BCA) + nanodrop (Fig. 2)
 - Total protein extracts from each region have been equalized and will be examined for differential expression of HSP70 by Western-Blotting (Fig. 3&4)
- Generation of mayfly salt-response curves
 - Site Selection – 10 Stream sampling sites will be determined through examination of water chemistry across the state using the PSU LoVoTECS network and fish sampling data from NH Fish & Game (Fig. 5)
 - Mesocosm aquaria mimicking stream environments will be used as housing in an attempt to limit handling stress (see Fig. 6)
 - Following three day acclimation period, nymphs will be exposed to a variety of salt concentrations
 - Total protein contents will be extracted and examined for levels of HSP70 expression corresponding to severity of salt treatment
- Quantification of in-situ HSP70 expression in NH streams
 - Specimen collection will occur once per month May-September with a goal of no less than 30 specimens per site, per month
 - To avoid any bias of stress-induction through handling/travel, individuals will be flash frozen in liquid nitrogen immediately following collection in the field
 - Each frozen specimen will undergo protein extraction identical to the previous experiments, expression levels of HSP70 will be compared to previously generated salt-stress response curves to examine correlations between habitats



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Literature Cited

- Doupe, R. G., & Horwitz, P. (1995). The value of macroinvertebrate assemblages for determining priorities in wetland rehabilitation: a case study from Lake Toolibin, Western Australia. *Journal of the Royal Society of Western Australia*, 78, 33-38.
- Hochachka, P. W., & Somero, G. N. (2014). *Biochemical adaptation*. Princeton University Press.
- Hyne, R. V., & Maher, W. A. (2001). Macroinvertebrate biomarkers: Links to toxicosis and changes in populations or communities. Cooperative Research Centre for Freshwater Ecology.
- Johnson, B. R., Weaver, P. C., Nietch, C. T., Lazorchak, J. M., Struewing, K. A., & Funk, D. H. (2015). Elevated major ion concentrations inhibit larval mayfly growth and development. *Environmental Toxicology and Chemistry*, 34(1), 167-172.
- Kennedy, A. J., Cherry, D. S., & Currie, R. J. (2004). Evaluation of ecologically relevant bioassays for a lotic system impacted by a coal-mine effluent, using *Isonychia*. *Environmental Monitoring and Assessment*, 95(1-3), 37-55.
- Lencioni, V., Boschini, D., & Rebecchi, L. (2009). Expression of the 70 kDa Heat shock protein family in Alpine freshwater chironomids (Diptera, Chironomidae) under natural conditions. *Journal of Limnology*, 68(2), 251-256.
- http://lovoteccs.blogspot.com/2015_05_01_archive.html
- Pond, G. J. (2010). Patterns of Ephemeroptera taxa loss in Appalachian headwater streams (Kentucky, USA). *Hydrobiologia*, 641(1), 185-201.
- Sørensen, J. G., Kristensen, T. N., & Loeschke, V. (2003). The evolutionary and ecological role of heat shock proteins. *Ecology Letters*, 6(11), 1025-1037.