

Caddisfly habitat occupancy in Churchill: Implications for subarctic biomonitoring using eDNA



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INTRODUCTION

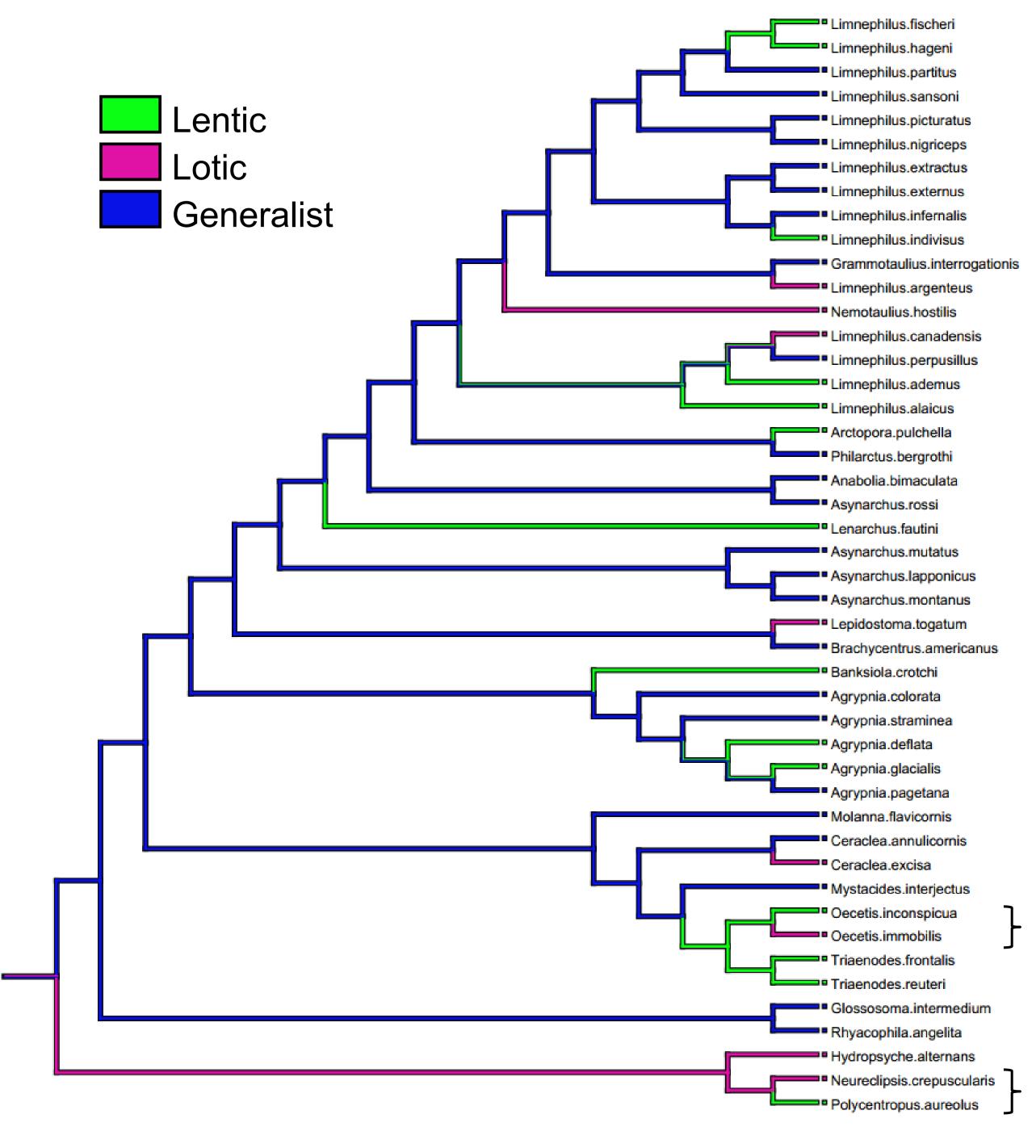
- Churchill, Manitoba is a model subarctic system with chronic stresses like seasonal floods and intense UV exposure (Serreze and Barry. The Arctic Climate System. 2009)
- Caddisflies (Trichoptera) are often used as freshwater indicator species because they are sensitive during their aquatic larval stage (Medeiros et al. Arctic. 2011)

QUESTIONS

- How does phylogeny affect habitat selection in these trichopteran communities?
 - Sister taxa often share adaptations for lentic (still) or lotic (flowing) habitats like case building and specialized mouthparts (Wiggins. Trichoptera. 1996)

How does this habitat choice shape eDNA

Sister species are rarely isolated!



 Biomonitoring using environmental DNA (eDNA) is promising but requires study in this system



- assay design in northern environments?
 - Implications on balancing the primer specificity vs sensitivity
 - Chronic stresses affect viability of genetic material in the water

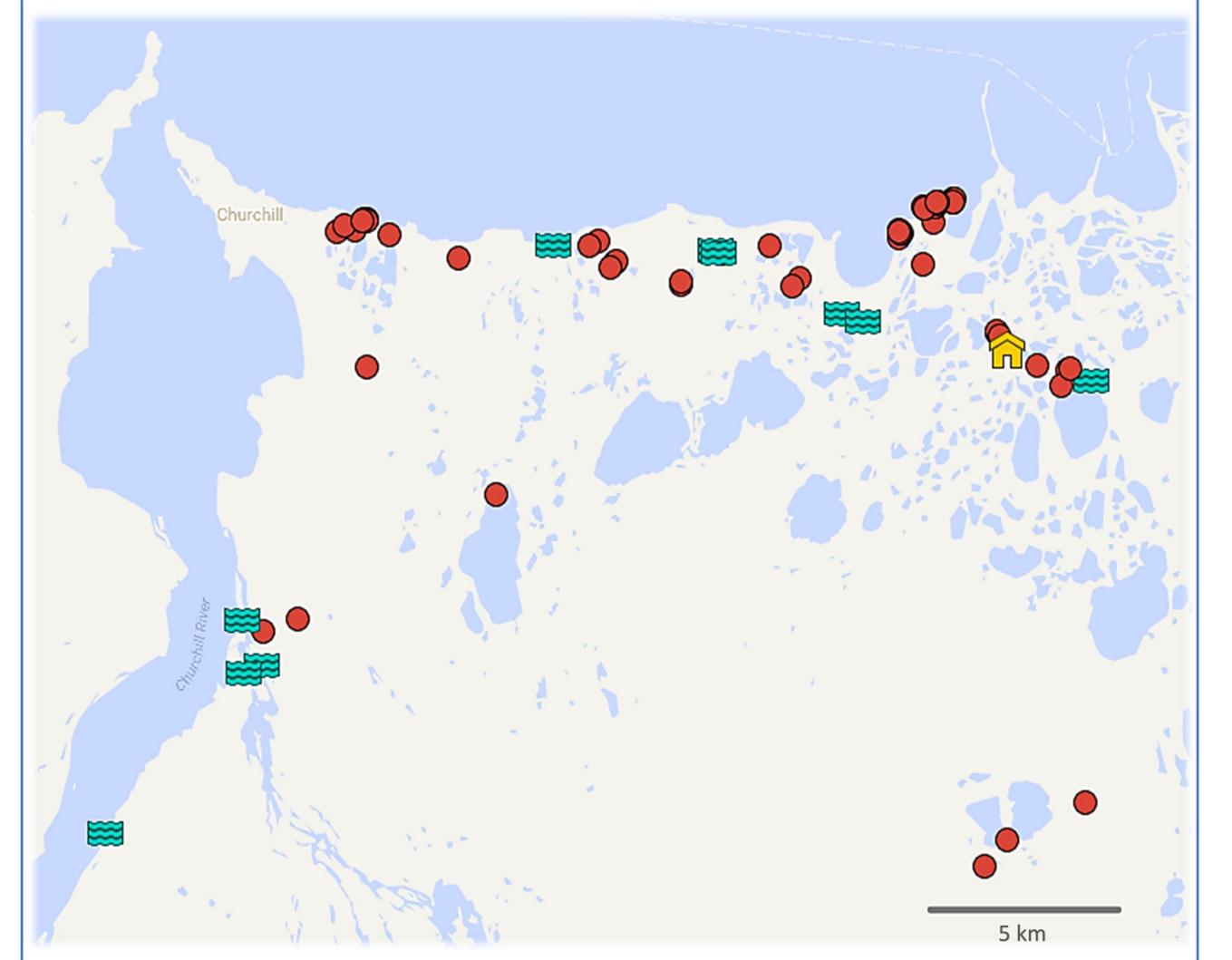


Figure 5: Churchill Trichoptera plotted on a phylogenetic tree built with COI, CAD, EF1- α , and POL-II genes where branch colours indicate habitat preferences. Green tips are lentic specialists, pink tips lotic habitats and in blue are species deemed generalists because they were captured in both habitats. Brackets emphasize sister species that are isolated from each other.

Figure 1: An example of this year's flood along the Churchill River

<u>qPCR vs METABARCODING</u>

- Metabarcoding is the "shot-gun" approach of sequencing everything in a sample
- Real-time polymerase chain reaction (qPCR) targets a single species and uses specific primers to amplify its DNA sequence
- qPCR has been shown to be as or more successful at detecting target species than metabarcoding (Harper et al. *bioRxiv.* 2017)
- qPCR is more sensitive to low concentrations of DNA (Goldberg et al. *Methods Ecol. Evol.* 2016)



Figure 3: A map of the 95 sites sampled for Trichoptera in 2017. In red circles are the lentic habitats (n=83) and in blue waves are the lotic habitats (n=12).

METHODS

- Repeated sampling done in 2010 and published by Boyle and Adamowicz (*PLoS ONE*. 2015)
- Sampled 20m in 95 sites census-style using kick-netting and hand-picking
- Morphological identification to species and confirmation via COI barcoding
- Phylogenetic reconstruction of habitat occupancy



<u>edna Implications</u>

- Primers will have be more specific than sensitive
- We need to investigate the rates of false positives and negatives in freshwater tundra systems while controlling for other factors that impact DNA degradation (like microbial activity, abundance of source organism, hydrology)
- We plan to use the Churchill biome gradient to test sites on both sides of the tree line



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