UNIVERSITÉ LAVAL

INSTITUT DE BIOLOGIE INTÉGRATIVE ET DES SYSTÈMES
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INTERLABS – IBIS

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I am currently pursuing a PhD in the laboratory of Jean-Sébastien Moore. I completed my master's thesis under the supervision of Louis Bernatchez. My research interests primarily center on conservation genomics and evolutionary biology, with a focus on salmonid species.

Unraveling the Evolutionary Significance of Sympatric Morphs of Anadromous Cisco (Coregonus artedi) Using Traditional Ecological Knowledge, Morphometrics, and Whole Genome Sequencing

Jeudi 5 juin 2025 à 12 h 30

Pavillon Charles-Eugène-Marchand, salle Hydro-Québec (1210)

Résumé:

Andromous cisco (*Coregonus artedi*) populations in Canada's James Bay and Hudson Bay represent unique evolutionary lineages that have long been central to Cree subsistence and knowledge systems. Among them, the most commonly harvested form, known to the Crees as *Nuutamesanio names*, undertakes a fall (September–October) spawning migration, forming the basis of annual community harvests. In contrast, the Cree community of Waskaganish has documented a second, lesser-known morph in the Nottaway River: *Kaachikaasuk names*, which spawns earlier in summer (July–August) and is locally recognized for its larger body size and distinctive appearance. In this presentation, I aim to show how traditional ecological knowledge is a crucial, yet often overlooked, component of conservation—particularly when delineating Evolutionarily Significant Units. To illustrate this, I integrate genomic and morphological analyses to investigate the evolutionary origins and ecological significance of anadromous cisco morphs identified through Cree traditional knowledge. Morphometric comparisons reveal striking differences between the two morphs in traits linked to swimming performance (e.g., fin length, caudal peduncle depth) and feeding ecology (gill raker counts). Otolith analysis shows that *Kaachikaasuk* individuals grow faster and reach larger maximum sizes. Whole-genome sequencing reveals marked genetic differentiation (Fst= 0.07) and identifies two large (~1 Mbp), non-recombining haplotype blocks associated with key ecological traits. Our results highlight how long-standing Indigenous knowledge can guide and enrich scientific discovery. This case study sheds light on the evolutionary processes that drive ecological diversity in northern fish populations—and emphasizes the power of Indigenous-scientific collaboration in uncovering hidden biodiversity.