Vita

Candidate's name: Josephine Ann Crichton

Universities
Attended: Red Deer College (2018)
        General Biology

        University of Alberta (2020)
        Bachelors of Science
        Ecology & Environmental Biology

        University of New Brunswick (2021)
        Masters of Science
        Biology

Conference Presentations:

59th Northeast Algal Symposium, 2021. An Analysis of DNA Metabarcoding Techniques on Rhodophyta (Red Algae) Biodiversity and Phenology in the Bay of Fundy.

60th Northeast Algal Symposium, 2022. Monitoring Red Algal Biodiversity Using eDNA Metabarcoding.

An Environmental DNA Metabarcoding Approach to Monitoring Red Algal Biodiversity

UNIVERSITY OF NEW BRUNSWICK

THESIS DEFENCE AND EXAMINATION

in Partial Fulfillment

of the Requirement for the Degree of
Master of Science

by

Josephine A. Crichton

in the Department of Biology

U.N.B., Fredericton, N.B.

Tuesday, September 5th, 2023
12:00 p.m.

Bailey Hall, Room 22 & via MS TEAMs

Examining Committee

Dr. Gary Saunders	Co-Supervisor
Dr. Adrian Reyes-Prieto	Co-Supervisor
Dr. Jason Addison	Internal Examiner
Dr. Audrey Limoges	External Examiner
Dr. Mike Duffy	Chair of Oral Examination

Abstract

Biodiversity monitoring is an important tool in ecosystem conservation as it can provide reliable detection of invasive species, indicate resilience after disaster, provide early warning signs of ecosystem collapse, and serves as evidence for successful management of resources or ecosystems. Despite biodiversity loss being one of our most critical conservation challenges, biodiversity monitoring in marine ecosystems is typically conducted using SCUBA-based visual surveys or molecular-assisted alpha taxonomic (MAAT) surveys, which have several limitations. This study compares red algal species richness and compositional diversity detected using environmental DNA (eDNA) metabarcoding to that detected using a typical MAAT survey. My aim was to determine if eDNA analyses provide a cost-effective and comprehensive alternative to traditional survey methods, and to improve upon the currently available reference libraries for red algae. The results of this study demonstrate that eDNA metabarcoding is a useful tool to help fill in gaps left by MAAT surveys by allowing for more frequent monitoring and detecting hard to identify species. Nonetheless, the results support a growing bank of literature suggesting that a combination of MAAT and eDNA methods remains the best approach for maximizing species detection.