From barcoding single individuals to metabarcoding biological communities:

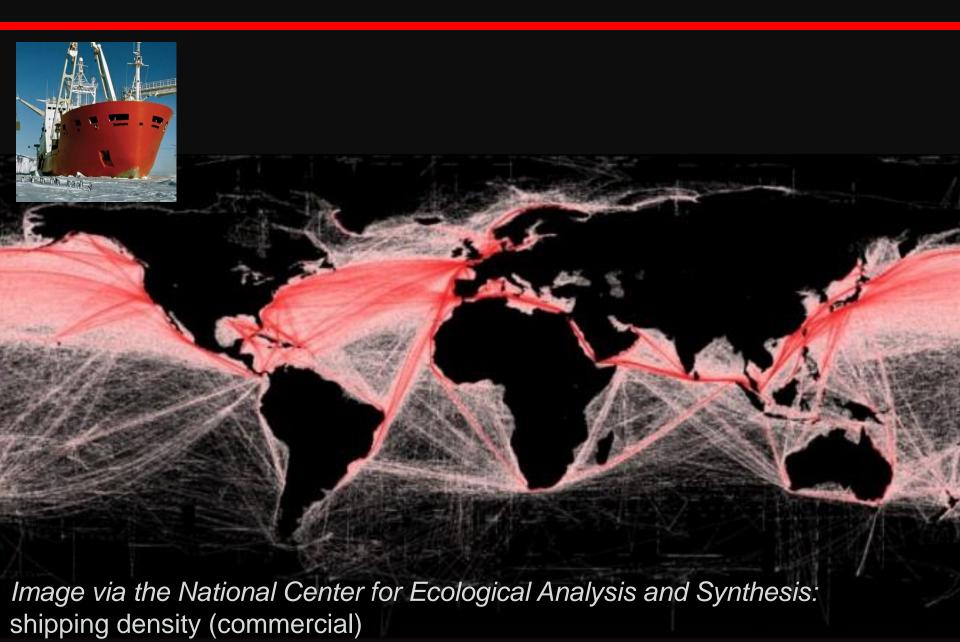
Towards understanding and managing invasive species



Global biotic homogenization



Global biotic homogenization



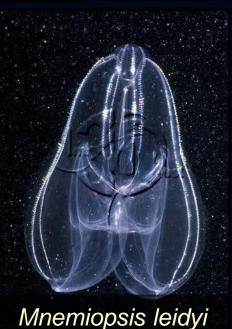
Aquatic Invaders the 'ecological villains'









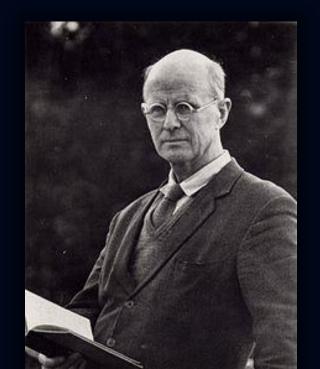






Living in a Changing World

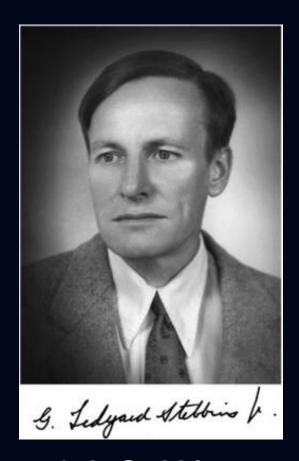
"Nowadays we live in a <u>very explosive world</u>, and while we may not know where or when the next outburst will be, we might hope to find ways of stopping it or at any rate damping down its force."



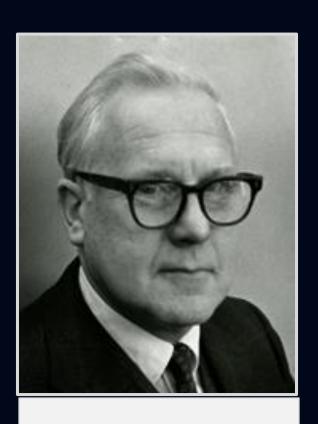
The Ecology of Invasions by Animals and Plants, 1958

Charles S. Elton 1900 - 1991

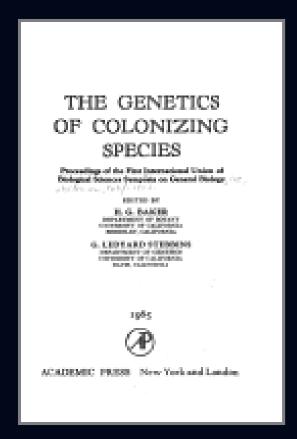
Living in a Changing World



G. L. Stebbins (1906 – 2000)



H.G. Baker (1920-2001)



(1965)

Using Genetic Tools

- ✓ The identify of aquatic invaders
- ✓ The evolutionary and invasion history
- ✓ Vectors of introduction and secondary spread
- ✓ Number of independent introductions
- ✓ Colonization dynamics across invaded areas
- ✓ Causes and consequences of invasiveness
- Early detection and preventive measures

Invasive Ascidians



- ✓ Native to European coastal waters
- ✓ Global distribution
- ✓ Major biofouler

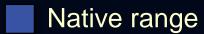






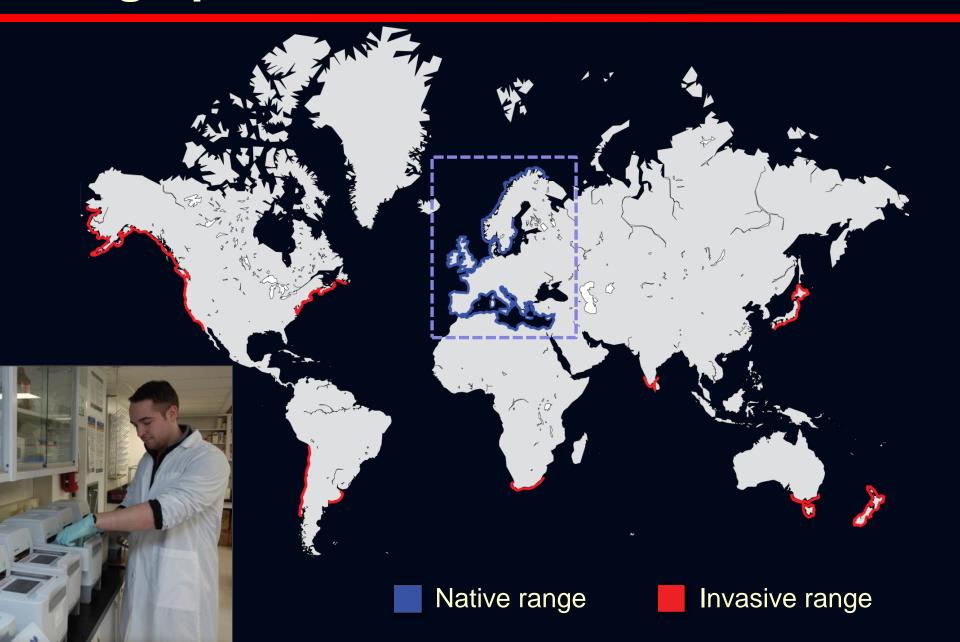
Geographic distribution of B. schlosseri

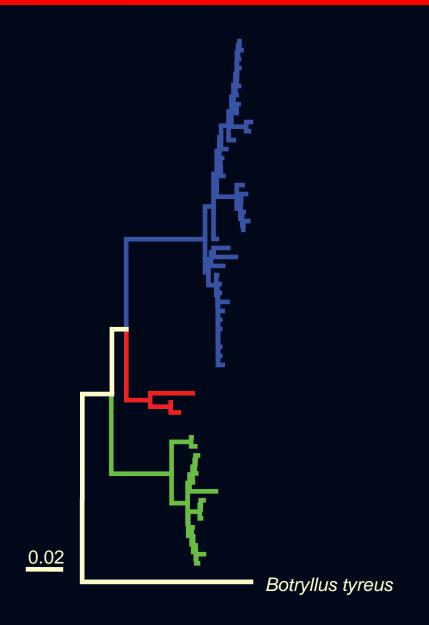


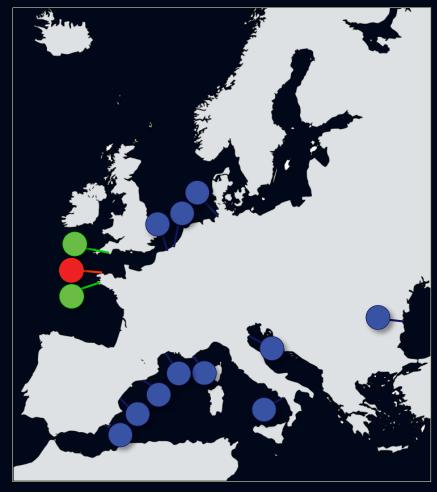




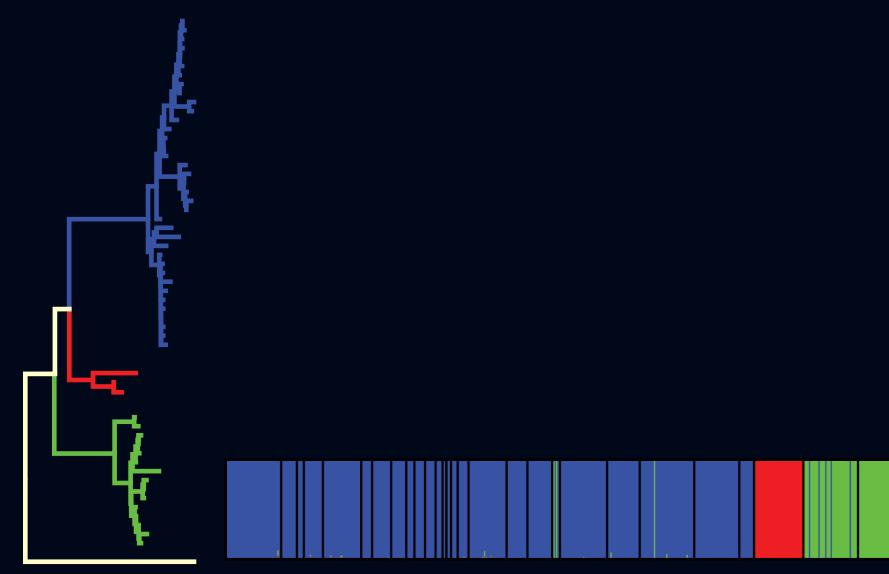
Geographic distribution of *B. schlosseri*

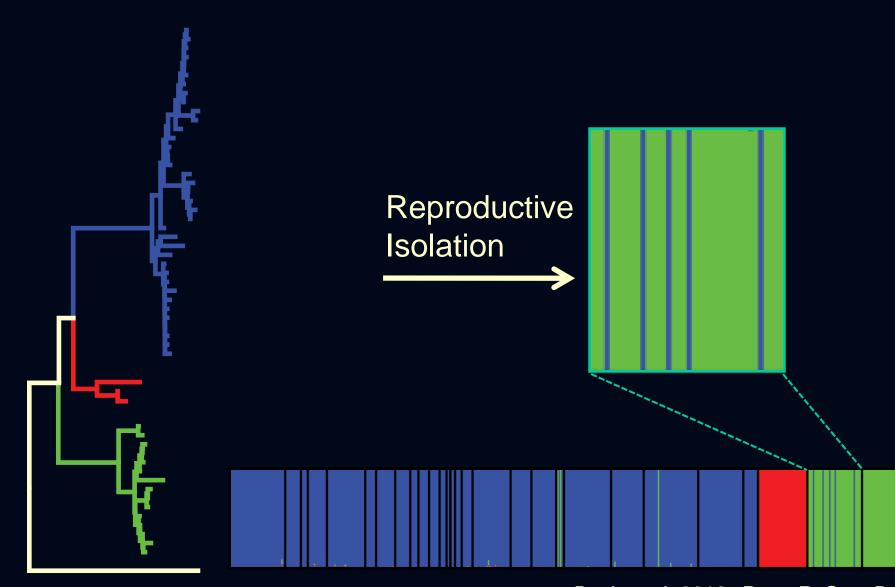






Bock et al. 2012, Proc. R. Soc. B





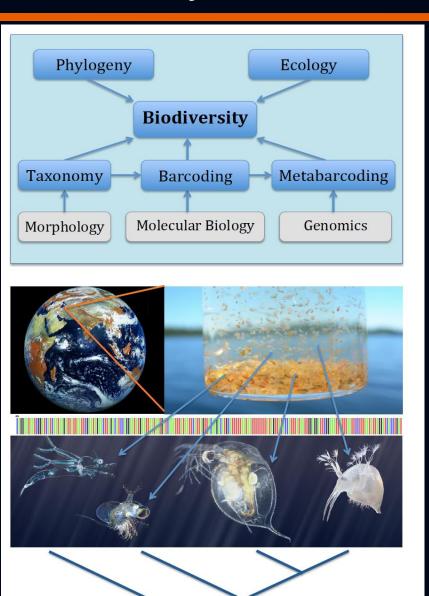
Bock et al. 2012, Proc. R. Soc. B

Why do some species proliferate at an alarming rate while their closest relatives are facing extinction?

Early detection of high risk aquatic invaders



Early detection of high risk invaders



Barcoding
+
NGS
=
Metabarcoding

Cristescu 2014 TREE

Mock communities



20 species

Brown et al. 2015 Ecol Evol

Mock communities



13 species

Brown et al. 2015 Ecol Evol

The impact of intra- and inter-specific diversity

- Simple communities (single individuals per species)
 generated a high correspondence of 60-84% between OTU
 number and species richness.
- When complex community were examined, this correspondence dropped to 31-63%.
- ✓ Intra-specific (or intra-individual) variation in the 18S marker sometime exceeds 3%.

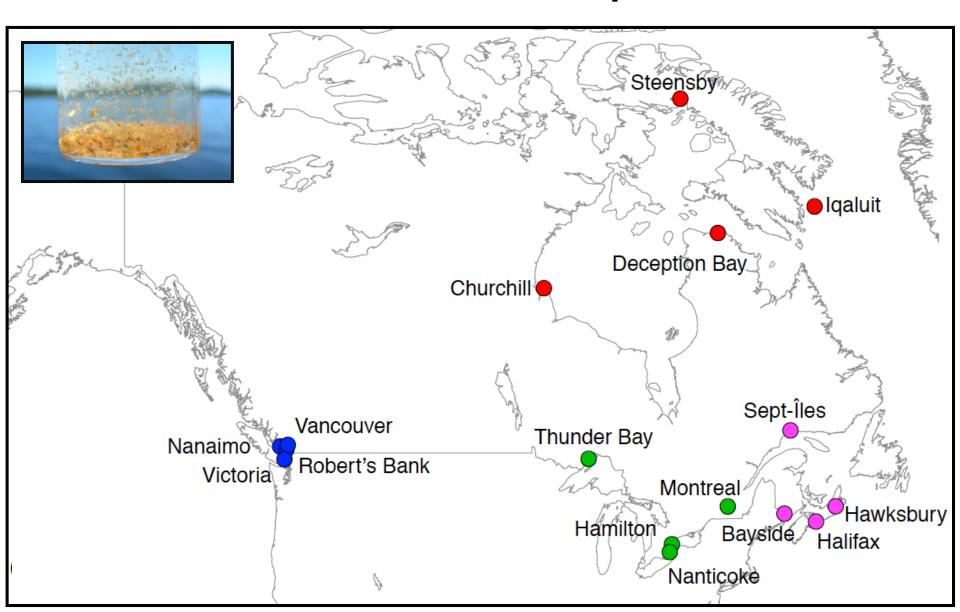
Brown et al. 2015 Ecol Evol

Evaluating different methods of clustering

- Stringent and relaxed filtering;
- Singleton sequences included and excluded;
- Three clustering algorithms (mothur, UCLUST, UPARSE);
- Three methods of treating alignment gaps.
- ✓ The number of OTUs varied by nearly three orders of magnitude;
- ✓ The use of relaxed filtering and the inclusion of singleton greatly inflated the number of OTUs.

Flynn et al. 2015 Ecol Evol

Spatiotemporal zooplankton biodiversity trends across 16 Canadian ports



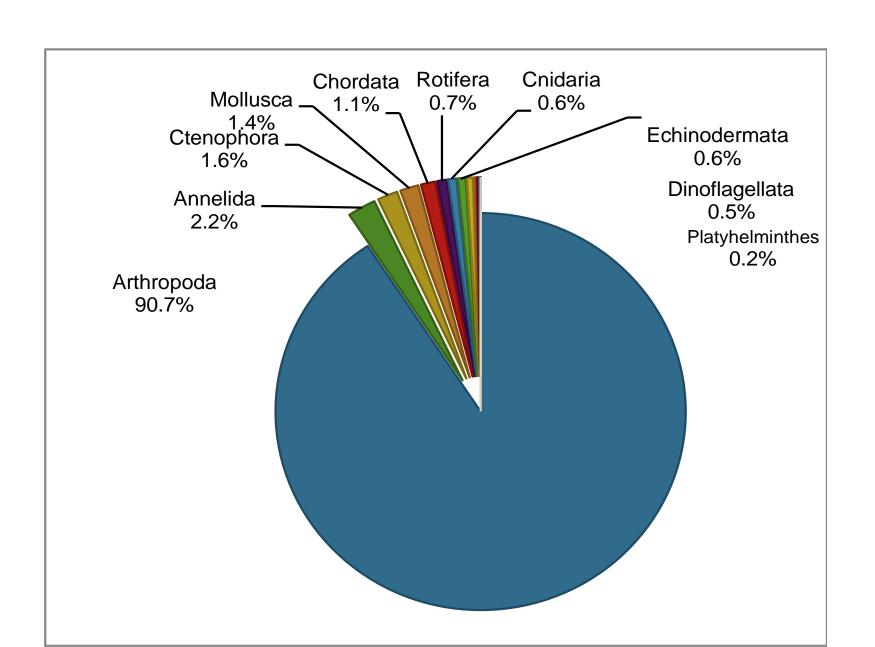
Methodology

The clustering approach	A taxonomy dependent approach
OTU clustering	Blast searches of individual reads against local databases
Requires a reliable barcoding gap and accurate divergence threshold	Requires a well developed reference library and concerted global effort
Validated methodology based on mock communities	Requires customized pipelines specific to the marker and taxa of interest
Taxonomic extension is facultative	Taxonomic extension is at the core of the approach

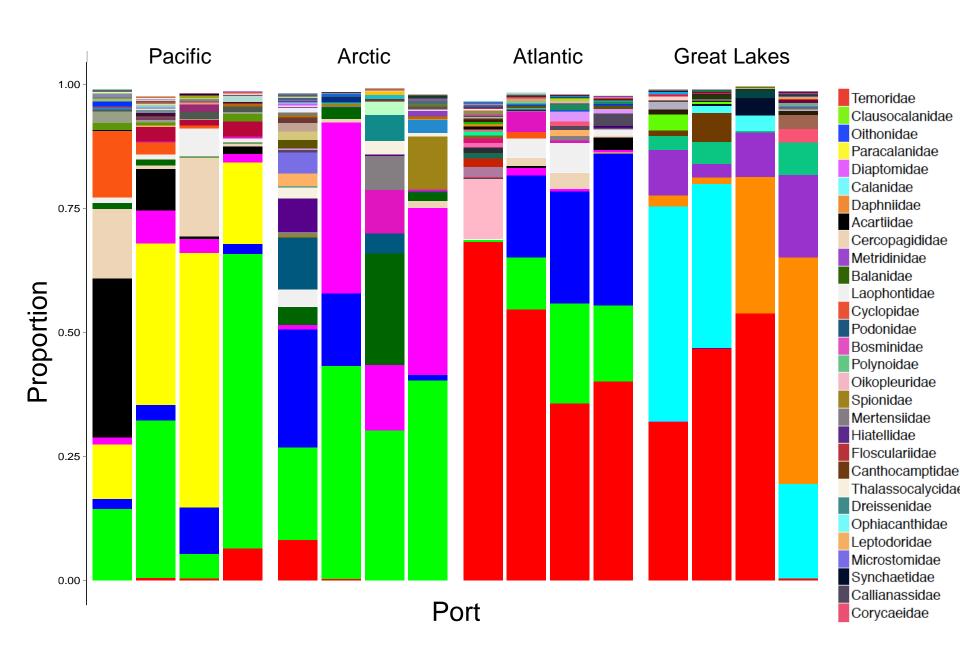
Highlights

- Taxonomic classification and phylogenetic inferences of over seven million sequences;
- Identified species spanning 392 metazoan families and 105 orders, complementing previous surveys based on morphological identification;
- Revealed species from over 30 orders that were previously not reported in zooplankton surveys;
- Certain taxonomic groups were underrepresented due to incomplete reference databases and low interspecific variation;
- Zooplankton communities were distinct among coastlines and among habitat types;
- Biodiversity varied substantially across seasons particularly for the subarctic region;
- Revealed a large number of NIS, many of them in previously unreported regions.

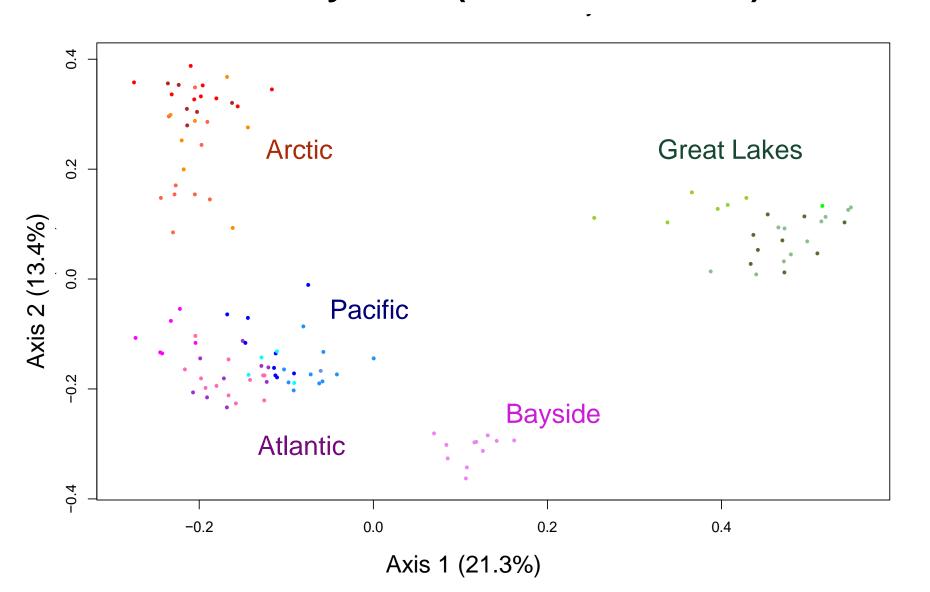
Proportional abundance of phyla across samples



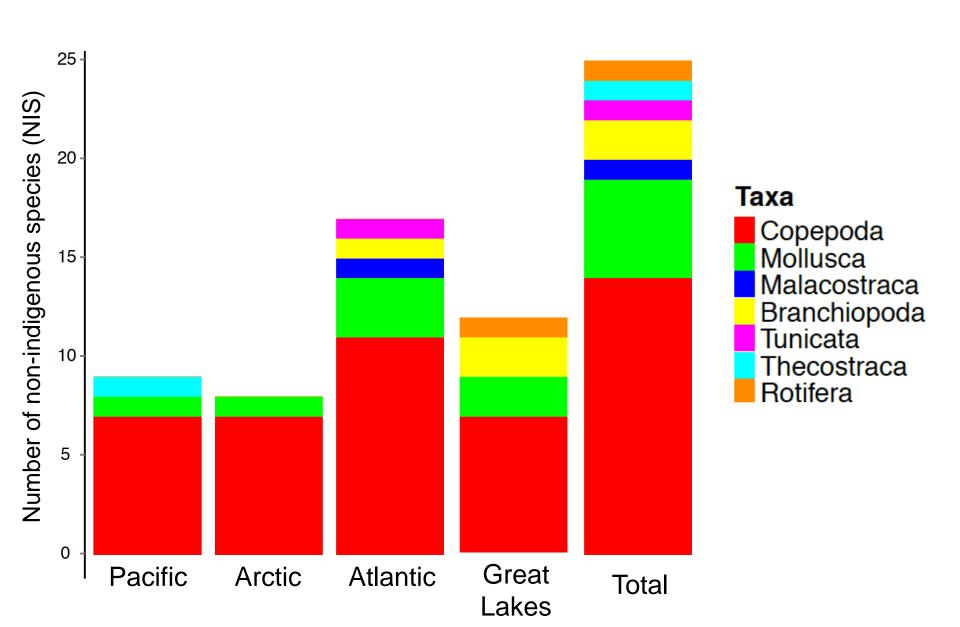
Proportional abundance of families across samples



PCA of sample (zooplankton composition) at the family-level (after rarefaction)



Identifying invasive species



Conclusions

The metabarcoding approach is very sensitive if applied appropriately

We need to farther advance:

- ✓ Reference libraries that incorporate reliable taxonomic information;
- ✓ Comprehensive databases of invasive species;
- ✓ Methodological validations using mock communities;
- ✓ Multi-marker approaches;
- ✓ Continue to promote standardization and reproducibility of metabarcoding approaches;
- ✓ Global coordinated effort that integrates traditional approaches and effectively implements the emerging technologies.

Aknowledgements

Lab members

Collaborators

- Hugh MacIsaac
- Teri Crease
- Cathryn Abbott
- Sally Adamowicz
- Paul Hebert













Barcoding as a Canadian Icon





An NRC Research Press Journal

