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Emma Taccardi

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Can stable isotopes indicate the geographical origins of sea lice?

Emma Taccardi^{1,2}

Carrie Byron³, Ian Bricknell^{1,2}

¹School of Marine Sciences & ²Aquaculture Research Institute, University of Maine; ³University of New England







Stable Isotope Analysis (SIA)

- Animal movement, food web dynamics, population differences
- Aquatic vs. terrestrial, marine vs. freshwater, inshore vs. offshore habitats
- Quantify origins of sea louse populations?



Objectives

- What is the most efficient protocol for sea lice SIA?
- Can wild and farmed populations of lice be identified in the wild?
- Analyze δ^{13} C and δ^{15} N values of lice from Atlantic salmon



Methods

• Lice collected from:

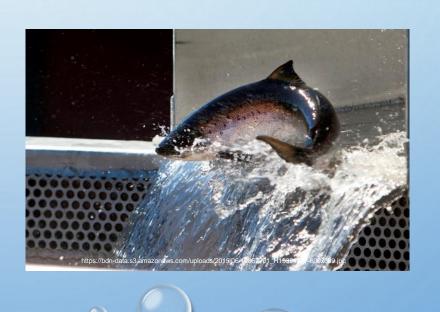
Farmed salmon in Cobscook Bay, ME

Wild salmon at Milford Dam, ME

Wild salmon at Milford Dam, ME

Processing: storage media; acidification





Methods







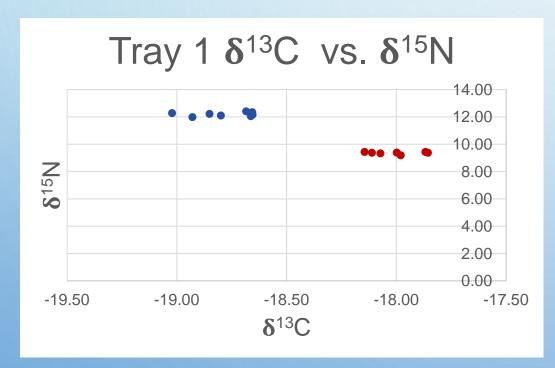


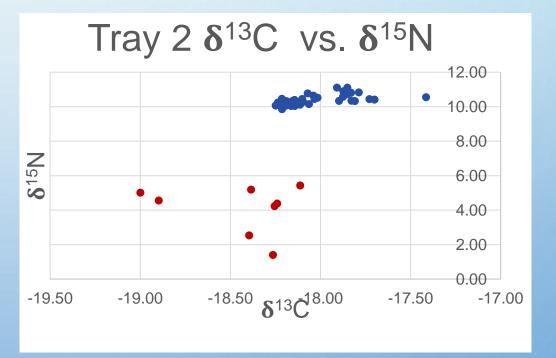
- Capsules analyzed at University of California, Davis
 Stable Isotope Facility
- Analyzed δ¹³C and δ¹⁵N with RStudio

Results

- All lice found on farmed salmon were L. salmonis
 - All lice found on wild salmon were Argulus foliaceus



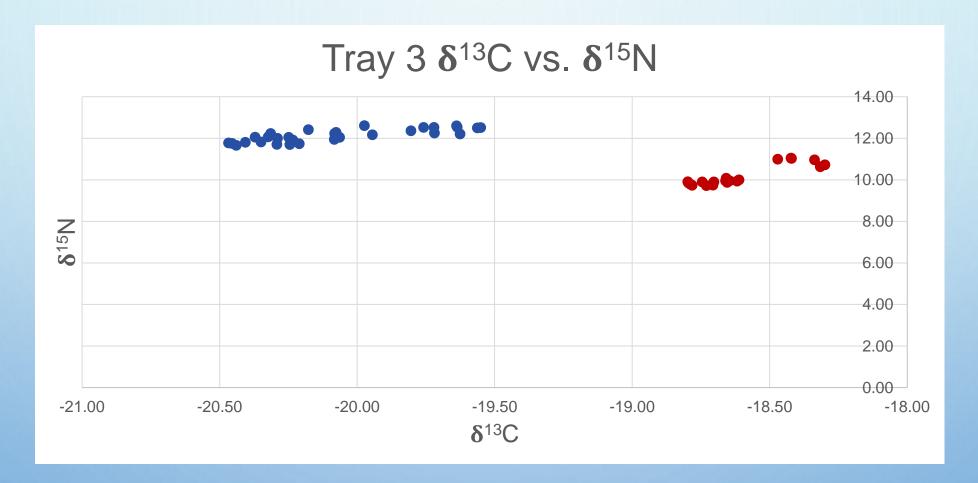




Seawater vs. DI Water

Acidified vs. Not Acidified

Results



Wild vs. Farmed Salmon

What does this mean?

- Processing significantly affects isotope signatures
- Lice signatures from farmed vs. wild salmon were unique
- Appears promising that isotopes will differ between other food sources for lice

Next steps...

- Compare sea lice and host isotopes
 - Fin, liver, skin, and white muscle
- UK samples
- Build detailed dataset and run multifactor ANOVA



Thank you!

Questions or comments?

emma.taccardi@maine.edu



















Schram, T.A. 1993. Supplementary descriptions of the developmental stages of *Lepeophtheirus salmonis* (Krøyer, 1837) (Copepoda: Caligidae). Pathogens of wild and farmed fish: sea lice. New York: Ellis Horwood. 30-47.