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Can stable isotopes indicate the geographical origins of sea lice?

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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 $\delta^{13}C$ and $\delta^{15}N$ values of lice from Atlantic salmon

Methods

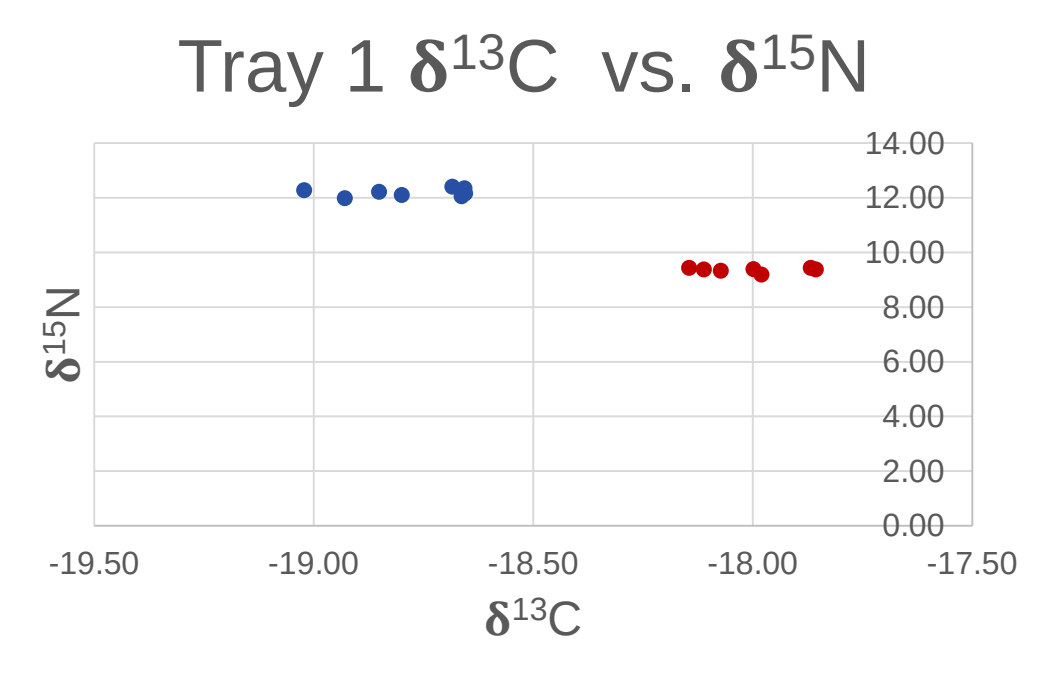
- Lice collected from:
  - Farmed salmon in Cobscook Bay, ME
  - Wild salmon at Milford Dam, ME
- Processing: storage media; acidification

Methods

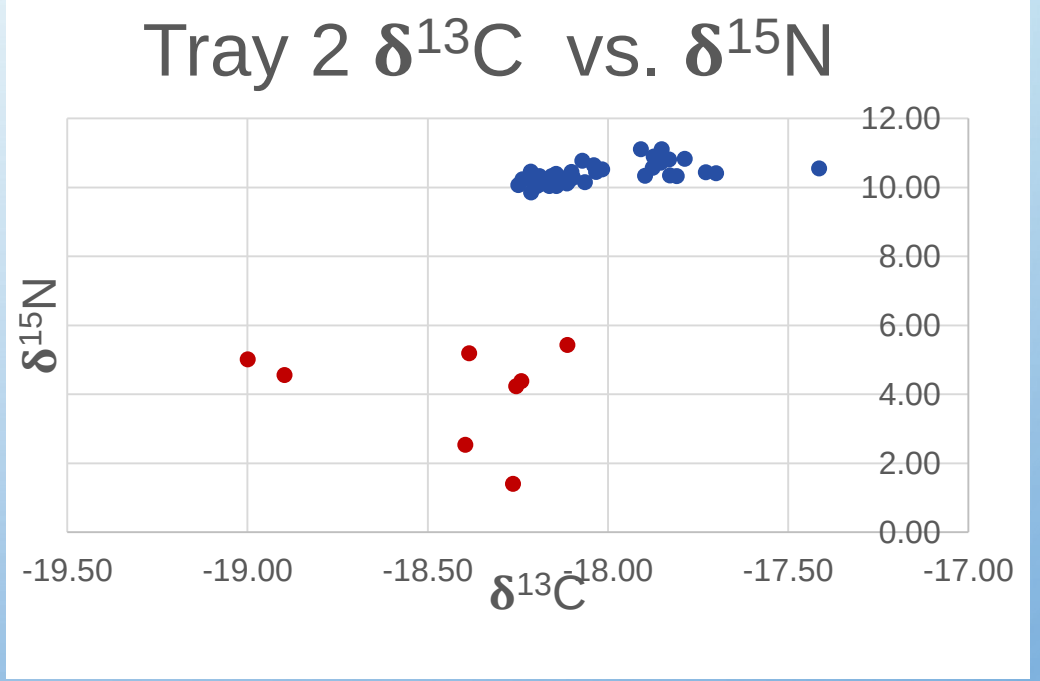
- Capsules analyzed at University of California, Davis Stable Isotope Facility
- Analyzed $\delta^{13}C$ and $\delta^{15}N$ with RStudio

Results

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

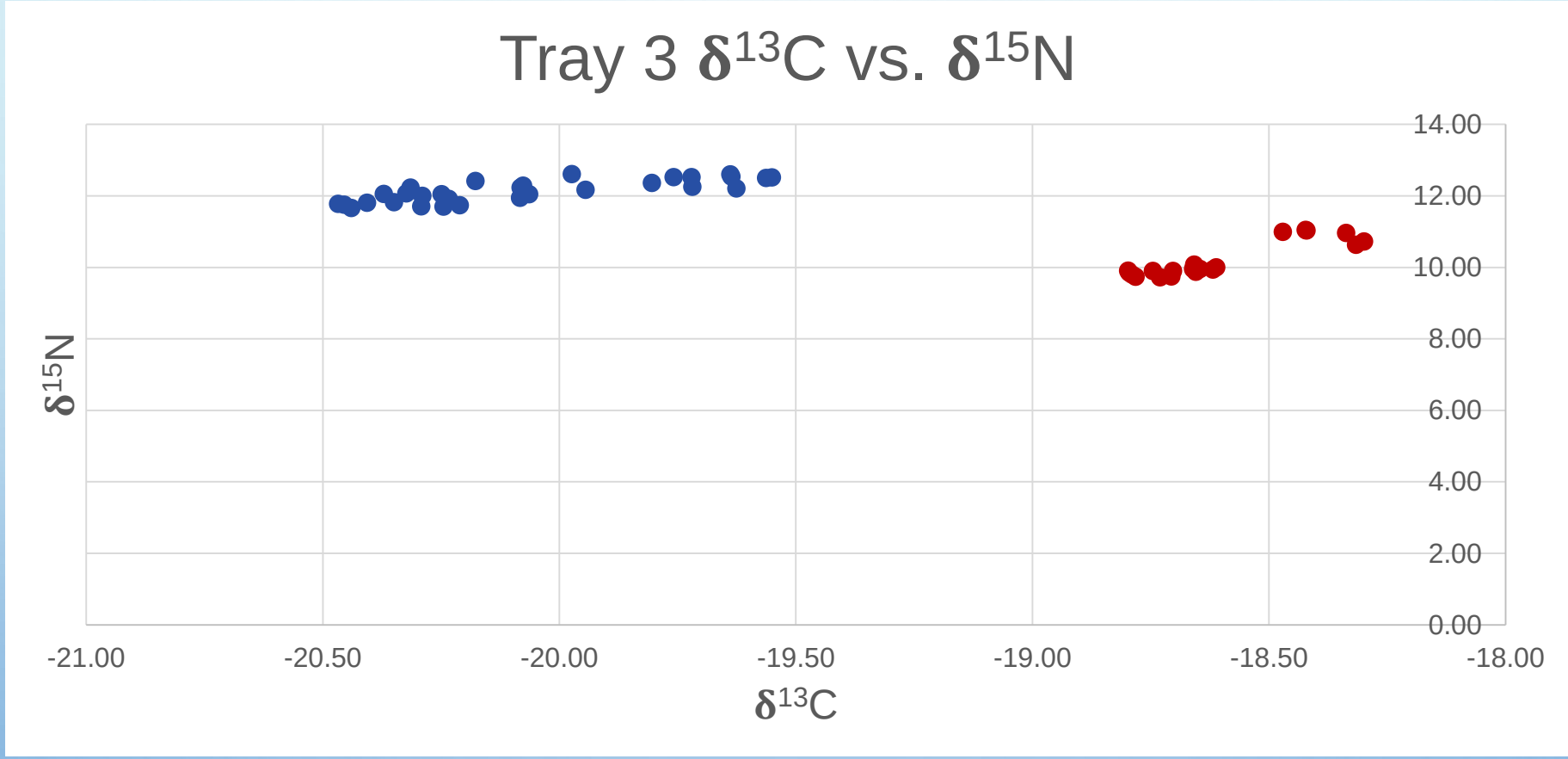


Seawater vs. DI Water



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?

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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.