

3-2015

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Recommended Citation

Short, Aidan W. and Carlon, David B., "A molecular analysis of green crab diets in Casco Bay, Maine" (2015). *Marine Lab Student Papers and Projects*. 12.

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A molecular analysis of green crab diets in Casco Bay, Maine

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A new wave of green crabs *Carcinus maenus* is sweeping through the Gulf of Maine (GOM). While first reports of green crabs in the GOM date from the early 1900s, populations in southern GOM have exploded in the last five years. In the Casco Bay region, this unusually high abundance is associated with poor commercial shellfish landings and the decline of eel grass habitat (*Zostera marina*). To determine the mechanistic roles green crabs play in direct and indirect ecological interactions, it is important to understand diet breadth, and how feeding preferences change in response to ecological context. Since green crabs are omnivorous, traditional approaches to diet analysis via hard parts suffer from substantial bias. We are using DNA barcoding and next generation sequencing (NGS) to analyze green crab diets from a longitudinal sampling design in Casco Bay. In addition to a temporal dimension, our design includes two habitats: clam flats and eel grass beds. We have now sampled ~ 1000 crabs and have processed 460 individual stomachs from a range of sizes and both sexes. Here we will present: our sampling design, our NGS pipeline, and preliminary analysis from a lobster-specific (*Homarus americanus*) probe.

Presenting author status: Undergraduate

Preferred presentation type: Poster

Preferred topics: 3. Biological invasions; 18. Molecular ecology

Benthic Ecology Meeting, 2015 Quebec City, Canada