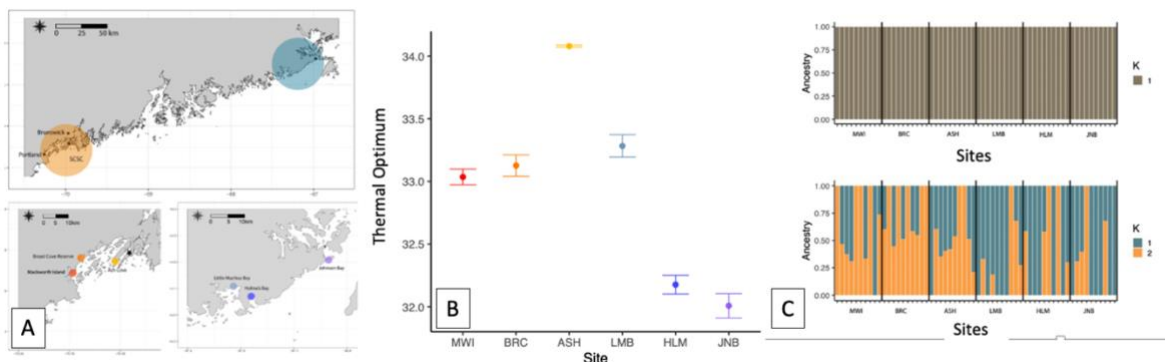


## Phenotypic divergence between sites in photosynthetic thermal response despite low genetic differentiation in Gulf of Maine *Ascophyllum nodosum*

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The ocean, and particularly the Gulf of Maine, is currently warming rapidly due to human-caused climate change<sup>1,2</sup>. These changes put coastal seaweeds at risk of reduced abundance, range shifts, and local extinction which threaten entire coastal ecosystems reliant upon them<sup>3</sup>. When attempting to understand contemporary changes and predict future shifts in organisms, it is important to consider the ways in which a species has evolved to deal with variation in environmental conditions throughout its range. Species which are locally adapted, that is ones which show genetically based differences in environmental adaptations matched to their local environment, can be more vulnerable to climate change compared to species which have plastic phenotypes that change based on local conditions. These differences are often not investigated<sup>4</sup>.

*Ascophyllum nodosum* is an intertidal seaweed found along the North Atlantic coasts, and it serves important ecological and economic roles. This project sought to determine if *A. nodosum* displays geographic variation in thermal performance and the population genetic processes potentially underlying this variation. To do this, I collected 10 individuals from six sites in the Gulf of Maine, three southern sites and three northern sites (Fig 1A). I then grew these samples in common conditions for three months, before performing an experiment to determine optimum temperature for photosynthesis for each site (Fig 1B). I found that some sites differed in thermal performance. I next sequenced the samples' DNA with funding by Grua/O'Connell Award. Initial analyses have revealed that there is high genetic connectivity between sites in the Gulf of Maine, and that genetic differentiation is low between sites.



**Figure 1. A)** Sampling regions and sites. **B)** Thermal optimum for photosystem II efficiency. **C)** ADMIXTURE analysis of genomic data. Similar support for 1 and 2 populations.

My genetic findings suggest that the differences in thermal optimum could be either due to long term epigenetic priming to temperature or adaption via small regions on the genome. With further analysis of the genomic data, I will gain more insight into these non-mutually exclusive alternatives, and future experiments will investigate these alternatives. Further, the finding of low differentiation across sites is unexpected. I will be presenting my findings at the national Evolution conference this summer, writing the results up in a manuscript for publication, and my results and draft genome will assist other *A. nodosum*, seaweed, and Gulf of Maine researchers.

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