Integrating genomics and metabolomics to understand climate change response in marine species

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Project Rationale:

Integrating evolutionary information with ecological modelling allows us to explicitly consider adaptive potential when predicting biodiversity response to climate change. Thus far, these methods have employed single nucleotide polymorphisms (SNPs) to survey genetic variation, but little work has been dedicated to exploring other types of 'omic variation that might be relevant to adaptive potential and climate change response. Additionally, these methods have focused heavily on terrestrial vertebrates and plants and are therefore lacking application in marine systems. Given that environmental stress impacts metabolic signatures within an organism, metabolomics could provide important information for this sort of predictive framework and nudibranch molluscs could be an ideal system for this work since they are rich in secondary metabolites.

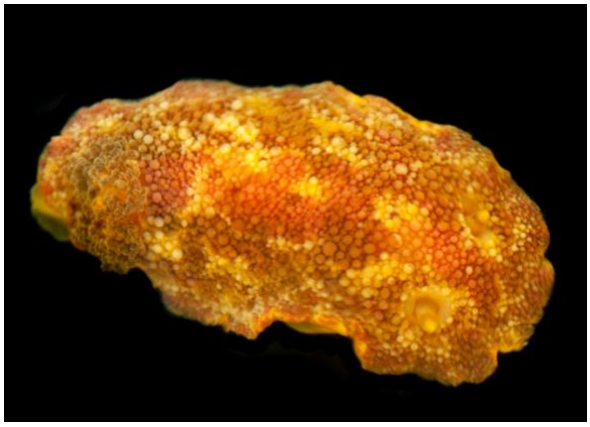

Figure 1: *Doris pseudoargus* from Väderöarna, Sweden housed in the Gothenburg Natural History Museum (photo credit: Klas Malmberg).

Project Activities: A total of 39 individuals of *Doris pseudoargus* (Mollusca: Gastropoda: Nudibranchia) (Figure 1) from 12 sites across Scotland, Northern Ireland, England, Ireland, Norway and Sweden were collected in the field or obtained from museum collections for this project. These collections cover a large portion of the species' range and span steep environmental gradients, providing ideal coverage for genotype-environment association analysis. The specimens also represented multiple colour morphs, ranging from yellow to mottled pink, demonstrating significant phenotypic variation in this species. High quality genomic DNA was successfully extracted from all individuals, including those collected in the 1990's and stored in <70% ethanol. DNA extracts were sent to Daicel Arbor Biosciences (Michigan, USA) for targeted sequencing following methods in Layton et al. (2020). An average of 9.0 million reads were recovered from the samples and nearly 85% of the reads had >99% accuracy. The reads have been trimmed and filtered and target sequences are now being extracted with a Python pipeline. Next, SNPs will be called for downstream analyses. Metabolite extraction and liquid chromatography-mass spectrometry of nine samples revealed similar metabolite signatures from all but one sample that may indicate a unique chemical compound that has not previously been isolated.

Ongoing Work: SNP data will be used for genotype-environment association analysis to identify a set of climate-associated outliers to be used in random forest-based forecasts of climate change response. Additional tissue is needed to supplement the material provided from natural history collections to complete the metabolomics work and integrate these signatures into our 'omics forecasts. The data produced here will support a DTP project (currently advertised) and will serve as pilot data for a Leverhulme application in 2023.