Deep-sea genomics: Elucidating the molecular mechanism behind extreme longevity in black corals

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Introduction

- Antipatharians, more commonly known as black corals, are long lived organisms with no recorded cases of cancer or tumor growths.[3]
- This species can inhabit oceans worldwide and has a broad range of depths they can survive at, yet most antipatharians are deep sea corals.[5]
- Hence, they are highly understudied and there are currently no publicly available nuclear genomes or transcriptomes for black corals.

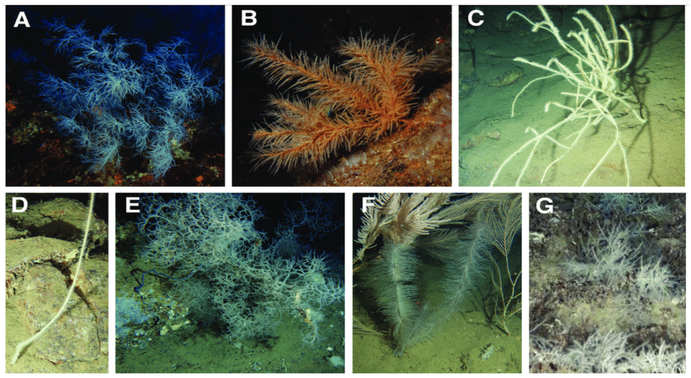

Fig. 1. Underwater images showing the broad morphology of black coral species: (A)Antipathella subpinnata, (B)Antipathella wollastoni, (C)Antipathes dichotoma (branched), (D)Antipathes dichotoma (whip), (E)Leiopathes glaberrima, (F)Parantipathes larix, (G)Phanopathes cf. rigida.[1]

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Background

- To resolve this aforementioned lack of information, we will, for the first time, sequence, assemble and annotate a black coral nuclear genome and transcriptome to reveal potential molecular mechanisms behind their extreme longevity and putative cancer suppression in these long-lived organisms.

Hypothesis

- We hypothesize that the black nuclear genome will be ~500,000,000 base pairs in size.
- We will utilize bioinformatics to scan the newly assembled and annotated black coral genome for proteins involved in a variety of known and predicted DNA repair mechanisms that are typically found in other organisms.

Experimental Plan

- Santiago Herrera (Lehigh University in PA) has a deep-sea research cruise to the Gulf of Mexico in August 2021 to an area where large *Leiopathes* colonies are known to occur.[2] He will be collecting fresh tissue from multiple individuals.
    - Tissue will be preserved in liquid nitrogen, a -80C freezer, ethanol, and RNAlater stabilization solution

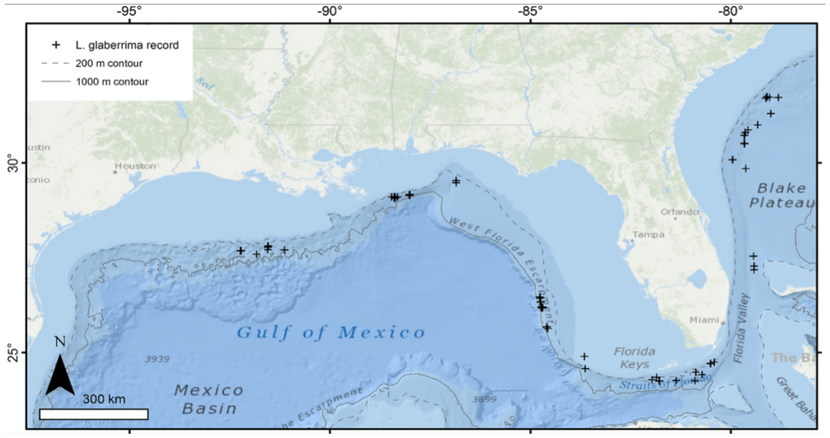

Fig. 2. NOAA's national database of deep-sea corals and sponges (NOAA 2016) map illustrating *Leiopathes glaberrima* (a long lived black coral that is common in the collection area) records.[4]

- The flash-frozen tissue will then be sent to Chris Mason at Weill Cornell Medicine in NYC where his lab is going to sequence the nuclear genome and transcriptome
    - DNA and RNA from freshly- collected specimens will be sequenced on the PromethION (long read technology to assist in assembling repeated/complex potions of the genome) and NovaSeq 6000 (transcriptome sequencing), respectively.
    - his bioinformaticians will assemble and annotate everything
- The assembled and annotated genome will be sent to Mercer Brugler (University of South Carolina Beaufort) to be mined
    - GenBank will be used to mine the genome by comparing the genes from the genome to other known genes related to preventing cancer
    - This information will then be used to infer functionality

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References

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