Biodiversity and Population Genetics of *Wirenia argentea* (Mollusca, Solenogastres)

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INTRODUCTION

Aplacophorans are a group of small, wormlike animals that are closely related to snails and other molluscs. While many other molluscs have shells, aplacophorans are covered in calcareous spines called sclerites. Aplacophorans consists of two classes: the Solenogastres, which number about 280 described species, and the Caudofoveates, with about 130 described species. They are ecologically and evolutionarily important, but their taxonomic diversity beyond the class level is not yet well known. There are only about 415 described species, but estimates indicate that there may be up to ten times as many yet to be identified[1]. Aplacophorans are already somewhat difficult to collect and study, as they are sometimes no more than a few millimeters long and found in deep water. Additionally, they are often similar in appearance, making morphological characteristics insufficient for identification. These factors all contribute to a lack of research currently being produced about this group.

Despite this lack of information, aplacophorans are ecologically important in deep-sea habitats[1] and crucial for understanding molluscan evolution[2]. The present study aims to assist in efforts to improve understanding of aplacophoran biodiversity and resolve aplacophoran phylogenetic relationships by conducting DNA barcoding from a large number of specimens collected from the Northeastern Atlantic Ocean near Iceland and Norway.

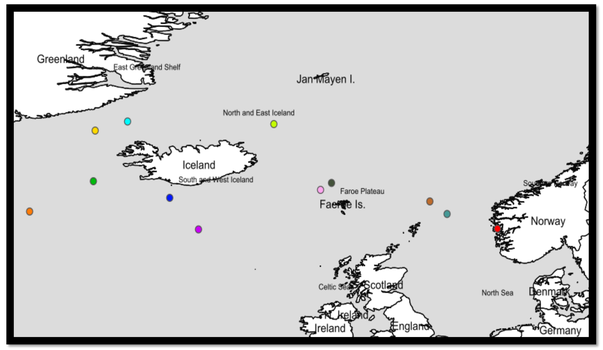
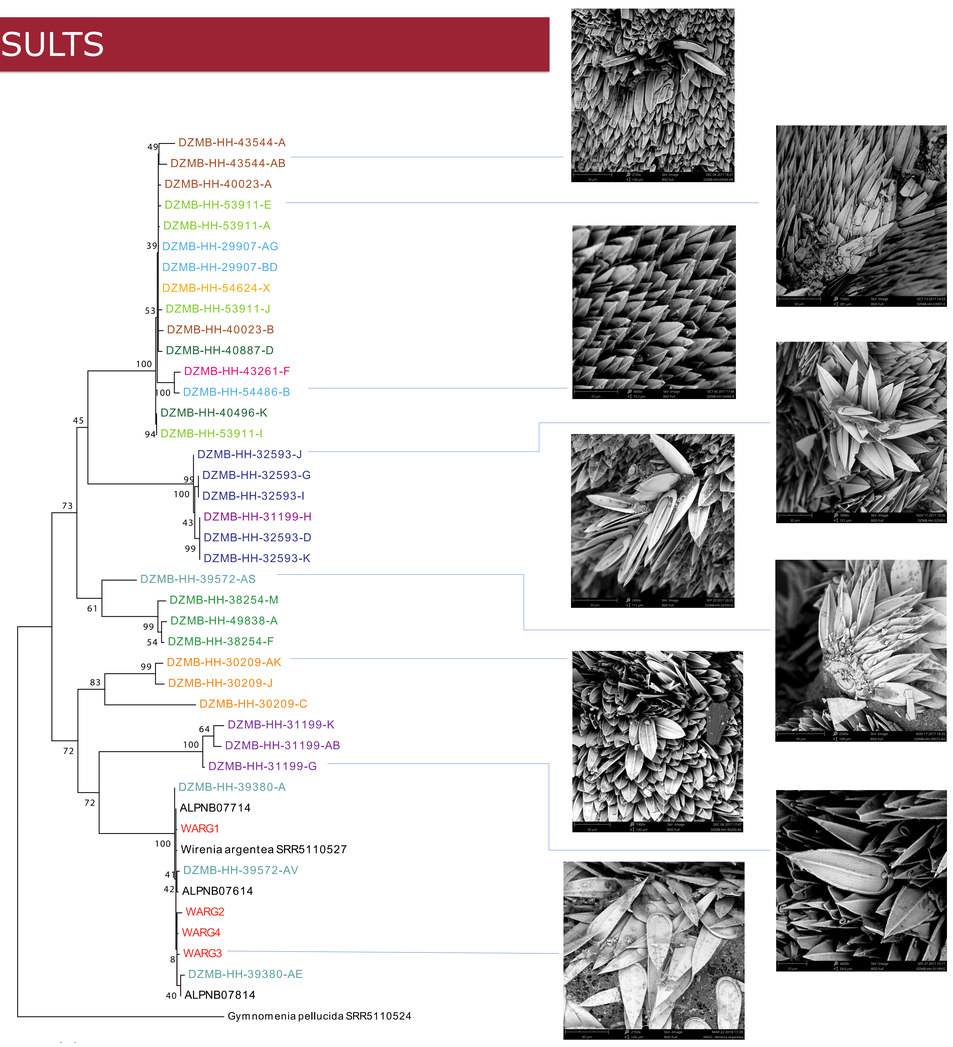


Figure 1. Each of the 12 sites plotted on a map. Site colors correspond with the phylogenetic tree.

METHODS

Specimens were collected during the IceAGE expeditions off Iceland and Norway. Scanning electron microscopy (SEM) was used to identify specimens of *Wirenia* (Solenogastres, Gymnomeniidae). At least five specimens from each site where *Wirenia* were selected for DNA extraction using the Omega Bio-Tek EZNA MicroElute Genomic DNA Kit. Polymerase chain reaction (PCR) with custom primers for the mitochondrial gene COI was performed for each extraction and then purified using the OmegaBio-Tek EZNA MicroElute Gel Extraction Kit. Purified PCR products were sent to the University of Arizona Genetics Core for Sanger sequencing. Sequences were assembled using Sequencher and aligned in MEGA7[3]. A phylogenetic tree was constructed using maximum likelihood in RaxML[4] using the GTR-GAMMA model with 750 bootstrap replications. The tree was rooted using Gymnomenia pellucida.

RESULTS



DISCUSSION

We recovered a largely well-supported phylogenetic tree. Initially, based on morphology of the calcareous sclerites covering the animals' bodies, we hypothesized that all of the specimens of *Wirenia* that we identified belonged to the described species *Wirenia argentea*. However, our preliminary results show as many as seven genetically distinct lineages that likely correspond to biological species exist in this region. These might be considered "cryptic species," species that are genetically distinct but morphology similar. However, re-examination of the scanning electron microscopy images reveal some differences among species.

Further research is needed to elucidate the evolutionary relationships between these groups and to determine whether or not they represent distinct species. Moving forward, we will sequence more individuals for COI and also sequence a second gene, 16S. We will also conduct histological sectioning to look at internal anatomy of representatives from each of these clades. Taken together, the results of this study shed light on the bidoversity and evolution of an understudied group of organisms.

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