

# INVESTIGATING GEOGRAPHICAL PHYLOGENETIC PATTERNS IN THE CHITON *TONICELLA MARMOREA* (MOLLUSCA, POLYPLACOPHORA)

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Poster Number: 299\_6

## Introduction

*Tonicella marmorea* (Fabricius, 1780) is a relatively large species of chiton (class Polyplacophora) reaching a length of 45 mm. The color of the mantle is usually red or green, often with yellow bands. This species can be found from lower tidal zone and down to 250 meters depth. It might appear in large numbers, grazing on organic material on the rock surfaces. It has an arctic circumboreal distribution, spanning the Arctic Ocean, the North Atlantic, and parts of the North East Pacific.

## Material and Methods

Sampling: Five station included Bergen, Trondheim, Bodø, Tromsø (Norway) and White Sea (Russia)

Separating the samples and observation of the morphological features under the light microscope

Taking pictures of samples

DNA Extraction: Dneasy Blood & Tissue kit

PCR amplification: Takara Ex taq HS

Sanger Sequencing

Sequences analysis via FinchTV, Genius and PopART softwares

## Results

All the obtained sequences were of good quality. There were a small number of variations between the nucleotide sequences from samples. Using the PopART software and TCS method, a haplotype network was drawn for the sequenced samples and four sequences of *Tonicella marmorea* from Canada. Based on this network, the maximum difference between the sequences from the studied samples was 11 changes.



Fig.1: Different appearance of specimens of *Tonicella marmorea*.

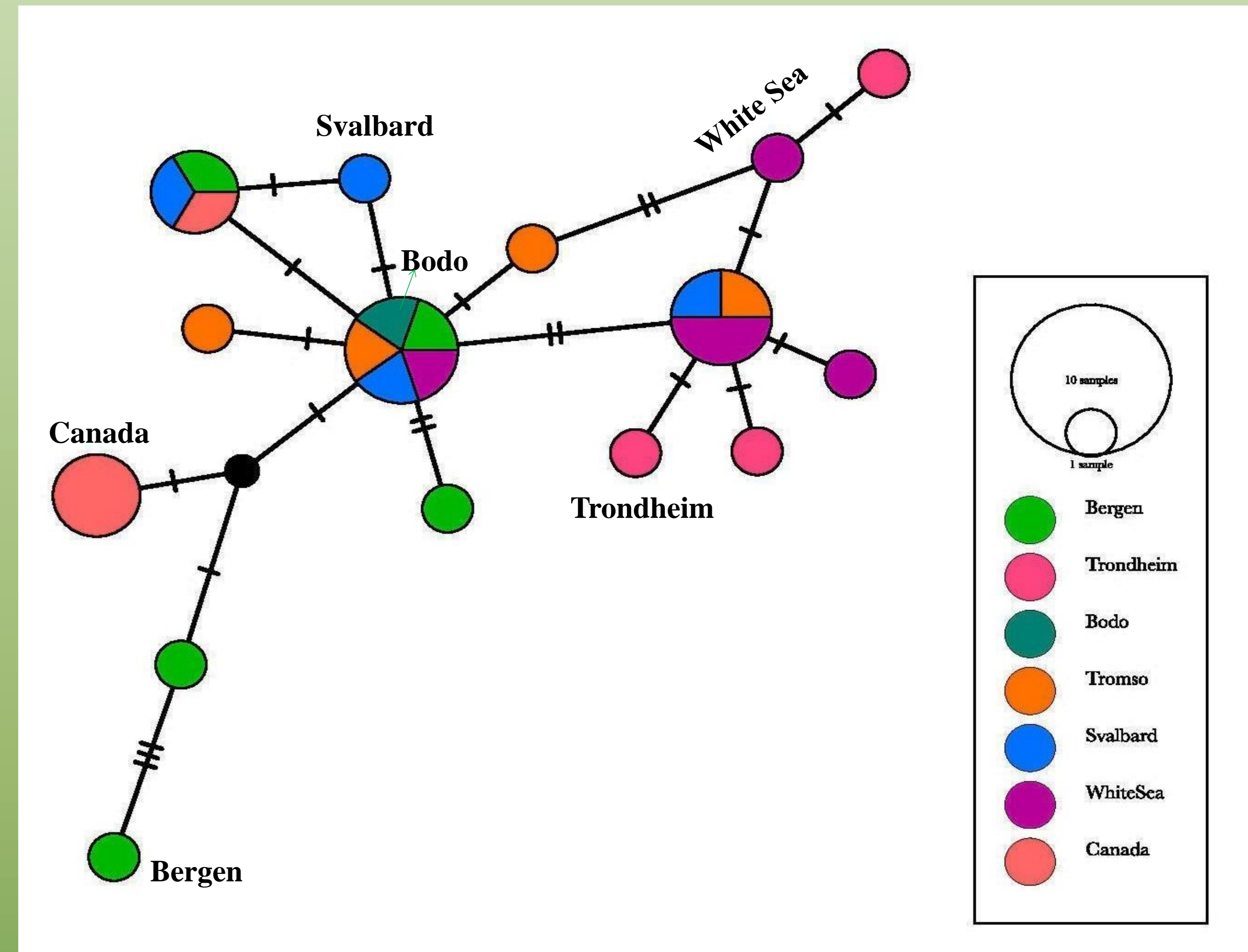


Fig.2: Haplotype network inferred from *Tonicella marmorea* mitochondrial sequences from Norway, the White Sea and Canada. Identical sequences are grouped together in a circle. The circle size indicates the number of samples that were found with each haplotype. The color indicate the different regions the samples were collected from. Each color represents a distinct region. Small dashed lines indicate the number of changes between sequences.

## Conclusion

Although the 22 studied specimens had small differences in the nucleotide sequences, there was no significant genetic difference between samples of this species in the five different coastal areas of Norway, and even the samples from Canada. This could mean that the expansion of this species to different places happened recently in geological time, not leaving enough time for changes to build up in the genome, or it could mean that there is ongoing gene flow between the different populations.