Depth-adapted Gene Discovery in Deep-sea Corals

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Introduction

Deep-sea corals (>200m depth) are subjected to harsh environmental conditions such as high pressure, extreme temperature, variable oxygen levels, and limited food source. Still little is known about the evolutionary processes in corals that enable them to be successful in such a broad scope of regions. Coral mitochondrial genomes have protein coding genes (PCGs) that are important to cellular energy functions. The ratio of nonsynonymous to synonymous substitutions, ω (dN/dS), of the mitochondrial genomes between deep and shallow species can therefore be a genetic marker of adaptation to the extreme environment of the deep sea[1].
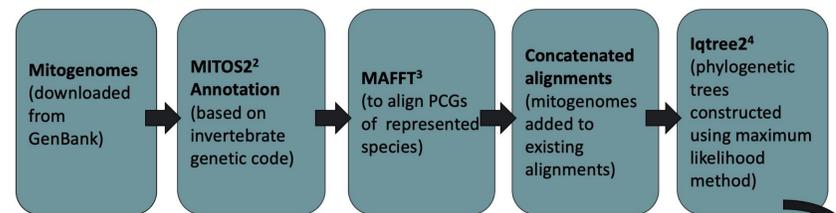

Scleractinia = stony/hard
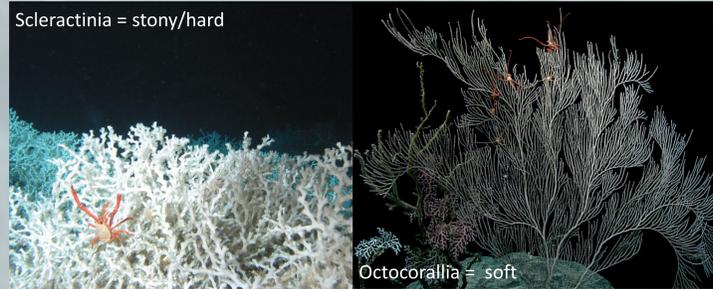
Octocorallia = soft

Images: NOAA Office of Ocean Exploration and Research.

Question

Will genes associated with cellular-energy functions be under positive selection (ω >1) across depth?

Methods

Mitogenome data collection & preparation:

Mitogenomes (downloaded from GenBank) → MITOS2[2] Annotation (based on invertebrate genetic code) → MAFFT[3] (to align PCGs of represented species) → Concatenated alignments (mitogenomes added to existing alignments) → Iqtree2[4] (phylogenetic trees constructed using maximum likelihood method)

41 species of Scleractinia (9 deep), 91 species of Octocorallia (28 deep)

Positive Selection Analysis: CodeML program in PAML package[5]

Table 1: Tests of selection conducted in CodeML

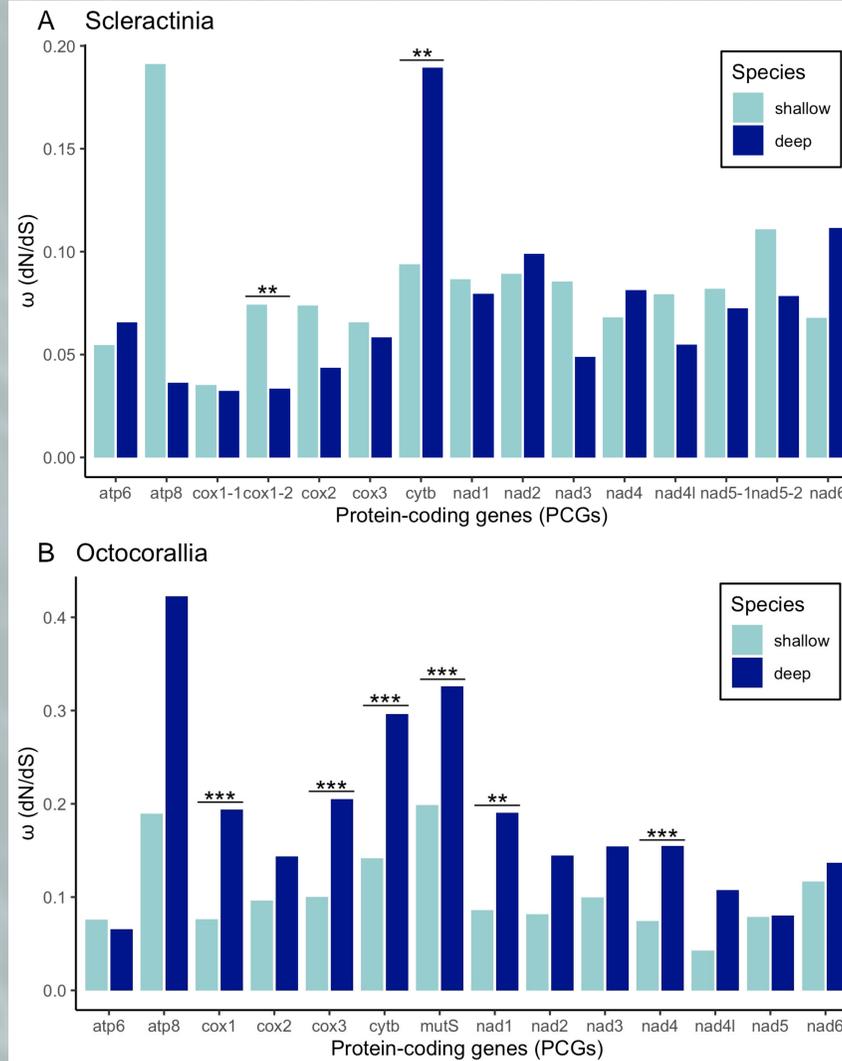| Models	Comparison	Test Description
Branch models	Two-ratio (M2) vs. one-ratio (M0)	Is the defined foreground (deep) branch more likely to have different ω from the background branch?
Branch-site models	Model A vs. Model A null	Is the foreground (deep) branch more likely to be under positive selection (ω > 1)

Results

A Scleractinia

B Octocorallia

Figure 1. Comparison of ω (dN/dS) by branch-model analysis. **<0.01, ***P<0.001. **(A)** 13 PCGs in Scleractinia mitochondrial genome with inserted intron in cox1 and nad5. **(B)** 14 PCGs in Octocorallia mitochondrial genome with MutS mismatch repair gene.

Table 2. Comparison of significant ω values for Octocoral nad1 gene between deep and shallow species identified by branch-site analysis.

Site Class	2a (ω < 1)	2b (ω = 1)
Shallow	0.04022	1.00000
Deep	16.37146	16.37146

Candidella imbricata
Radicipes sp.
Acanella sp.
Chrysogorgia tricaulis
Anthothela grandiflora
Nephthyigorgia sp. *

Figure 2. Portion of translated multiple sequence alignment for Octocorallia at possible site of positive selection. *shallow

Table 3. Sites under positive selection in the deep lineage by Bayes Empirical Bayes (BEB) analysis.

Gene	Codon	Amino Acid	BEB Values
nad1	109	I	0.999
	101	V	0.951

Results

- All ω values of mitochondrial PCGs for Scleractinians and octocorals < 1.
- **Scleractinia**: significant ω differences in genes cox1-2 and cytb
- **Octocorallia**: all ω values of PCGs in deep species branch were greater than shallow, except for atp6, six of which were significant.

Branch

- **Scleractinia:** no significant differences between Model A and null
- **Octocorallia:** Deep-coral are under positive selection in nad1 (ω = 16.37146) when shallow-coral are under purifying and neutral selection (ω < 1, ω = 1)

Branch-site

Discussion

- Scleractinians and octocorals are under strong purifying selection. Deep-sea octocorals exhibit a relaxed purifying selection.
- Positive selection can occur at select sites, but it may be undetectable as most sites are undergoing purifying selection[1].
- Scleractinia samples contain three "Basal"[6] species with greater divergence that could impact ω.
- Ratio of foreground to background species is uneven, may be reducing power to detect selection.
- Appears to be inherent differences in groups of coral
  - Scleractinia has introns in mitogenome
  - Octocorallia has MutS in mitogenome
- Evidence for positive selection in NADH dehydrogenase complex is seen in mammalian and other deep-sea invertebrate mitogenomes[1,7].

Future Direction
- Conduct M1a and M2a analysis on codeml[5]
- Omit high divergent species
- Obtain more deep-species mitogenomes

NOAA Office of Ocean Exploration and Research.

References & Acknowledgements

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Background image: NOAA Office of Ocean Exploration and Research.