Is molecular evolution faster in the tropics?

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Abstract

This study analyzed public DNA barcode sequences from the cytochrome c oxidase subunit I (COI) gene for six of the largest animal phyla (Arthropoda, Chordata, Mollusca, Annelida, Echinodermata, and Cnidaria) and paired latitudinally-separated taxa together in an automated fashion to explore latitude differences in molecular rates. Of 8030 lineage pairs, 4146 (51.6%) displayed a higher molecular rate in the lower-latitude lineage, while 3892 (48.4%) exhibited a higher rate in the higher-latitude lineage. Overall, only a weak trend was found supporting higher rates of COI evolution in lineages inhabiting the tropics compared with those inhabiting cooler regions. This weak pattern suggests that the Evolutionary Speed Hypothesis (ESH) may not serve as a strong universal mechanism underlying the latitudinal diversity gradient and that COI molecular clocks may generally be applied across regions.

Introduction

The ESH – Evolutionary Speed Hypothesis suggests that molecular evolutionary rates are higher among species inhabiting warmer environments vs species inhabiting cooler environments. Previous studies on the ESH (Wright et al., 2010, 2011; Gillman et al., 2009, 2012) have mainly looked at vertebrates using small numbers (<100) of latitudinally-separated species pairs to assess molecular rate differences. We aimed to broaden this species pair approach (Fig. 1) to span Annelida, Arthropoda, Chordata, Cnidaria, Echinodermata, and Mollusca.

Question: Do animals inhabiting tropical environments evolve at faster rates than animals inhabiting temperate environments?

Methods

A bioinformatics approach: a novel pipeline in R was developed to perform wide-scale phylogenetic comparisons of animal barcode data from BOLD: Barcode of Life Data System. Code developed: https://github.com/m-orton/k-Scripts/

Use of the Barcode Index Number (BIN): an operational taxonomic unit that closely corresponds to species and uses curated cytochrome c oxidase subunit I (COI) sequence data from animal specimens. BINs were used in place of species for the determination of species pairs.

Results

Fig 1. Latitude-Separated Species Pairing:
Tropical species exhibiting longer branch length than temperate species when compared with the outgroup, indicating a faster rate of evolution in the tropics.

Discussion and Conclusion

We observed a weak pattern of higher molecular rates in tropical species, with 51.6% of species pairs showing faster evolution in the tropics. This pattern suggests that the ESH may not serve as a strong universal mechanism underlying the latitudinal diversity gradient and that COI molecular clocks may generally be applied across tropical and temperate environments.

References


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Bioinformatics Pipeline Process

Data Download
Barcode sequences, taxonomic data, and geographic coordinates downloaded from BOLD and imported into R.

Sequence Filtering
Filtering sequences for minimal N content and sequence length (400 bp – 1000 bp).

Representative Sequence
Centroid sequence was determined for each BIN: minimum average pairwise distance to all other sequences within a BIN.

Alignment
Aligned sequences with MUSCLE (Edgar, 2004).

Genetic Distance
Calculated according to the TN93 model (Tamura and Nei, 1993).

Species Pairing
MN-alignment of latitude separation, 0.02-0.15 sequence divergence. Latitudinal ranges of ingroup species could not overlap by more than 25%.

Outgroup
Inclined, larger sequence divergence, fewer species pairs to assess molecular rate differences. We assessed the statistical analysis of pairwise rates looking for significantly more than 50% positive signed branch length ratios using a binomial test. Also testing if median signed ratio differed from a null expectation of 0 using a Wilcoxon signed rank test.

Biological Question:
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