The effects of ecological traits on the rate of molecular evolution in ray-finned fishes: a multivariable approach

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Abstract

Background: A myriad of environmental and biological traits have been investigated for their roles in influencing the rate of molecular evolution. However, most studies have focused on a single, trait, and few have considered multiple traits. Molecular rate may be measured by comparing the substitution rate of organisms that differ in a certain trait (Fig. 1). The objective of this study is to construct a bioinformatics pipeline that illustrates the effects of multiple ecological traits on the rate of molecular evolution in fish (including both previously investigated and novel traits).

Introduction

- Ecological traits have been investigated for their role in influencing the rate of molecular evolution. However, many studies are limited to a single trait, and few have considered multiple traits.
- Molecular rate may be measured by comparing the substitution rate of organisms that differ in a certain trait (Fig. 1).
- The objective of this study is to construct a bioinformatics pipeline that illustrates the effects of multiple ecological traits on the rate of molecular evolution in fish (including both previously investigated and novel traits).

Materials & Methods

- Fish COI sequences downloaded from Barcode of Life Data System (BOLD) database.
- Barcode Index Numbers (BINs) used as proxy for species.
- Data for 32 traits obtained from FishBase. Rates of molecular evolution quantified as branch lengths.
- Single-variable and multivariable regression analyses performed using traits as predictors and branch length as response variable. A bioinformatics pipeline was constructed in the R programming language. It is comprised of five main sections of code.

Results

Figure 4: Select single-variable regression results showing the effects of a) age at maturity (n = 331, p-value < 0.0001, R² = 0.25), b) longevity (n = 663, p-value < 0.0005, R² = 0.18), c) maximum body length (n = 3339, p-value < 0.001, R² = 0.12) and d) latitude (n = 4763, p-value = 0.0004, R² = 0.09) on branch lengths estimated using all three codon positions and controlling for phylogeny and number of nodes.

Table 1: Best-fit multivariable models after backwards selection process (n = 175), accounting for phylogeny. Bold p-values indicate significance at 0.05 level.

Conclusions

- The strongest predictor of molecular rate was age at maturity, which provides evidence for the generation-time effect in fishes.
- A non-significant trait effect in the multivariable analyses suggests that temperature-driven molecular rates do not appear to be a universal attribute across ectothermic groups.
- These results provide evidence for the importance of life history traits in controlling evolutionary rates in fish COI.
- The bioinformatics pipeline designed for this study may be adapted to investigate trait correlates in novel taxonomic groups.

References


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Github link to pipeline: https://github.com/jmay20/phylo.