

Molecular evolution of echolocation genes in cetaceans and bats

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Abstract

This study aims to understand the molecular evolution of hearing genes associated with echolocation in dolphins and bats. The convergence between these groups suggests that TMC1 gene is central to the evolution of echolocation and a case of convergence occurring on a molecular level.

Key words:

echolocation, molecular, convergence.

Introduction

Echolocation is a complex biosonar that evolved independently in cetaceans and bats, allowing them the production, emission and processing of high frequency sounds for spatial orientation. Among cetaceans, all odontocetes echolocate, sharing the same sound production and reception apparatus. During their radiation, this feature is thought to be under strong selection, especially with the invasion of freshwater systems and the recolonization of marine ecosystems. As for bats, almost all present laryngeal echolocation, except for the family Pteropodidae, where this sensorial trait was lost in most members and evolved secondarily in one genus of tongue clicking bats.

There is widely documented molecular convergence throughout the genome of both groups, especially for genes associated with hearing and cochlear development^{1, 2, 3, 5}. Our main goal was to investigate the molecular evolution of SLC26A5, TMC1, CLDN14, CDH23 and SMPX genes between odontocetes and bats. These genes are required for function and development of hair cells specialized in high frequency hearing, and some of them are under positive selection in odontocetes^{4, 5}, indicating that they may have an important role in the evolution of bats as well as marine and freshwater dolphins. We hypothesize that molecular convergent evolution may have occurred between dolphins and bats for hearing genes involved in echolocation.

Results and Discussion

As a preliminary investigation to identify potential study targets, we retrieved the sequences of SLC26A5, TMC1, CLDN14, CDH23 and SMPX genes for mammals in GenBank and generated phylogenetic consensus trees for the nucleotide and protein alignments of each gene. Early results from protein alignment of TMC1 (Img.1) show echolocating dolphins and larynx echolocating bats as sister groups, with *B. acutorostrata scammoni* (non-echolocating cetacean) as an outside taxa, while non-echolocating and tongue click echolocating bats are grouped together in a separated clade.

These findings suggest convergence of the coding sequence of TMC between echolocating dolphins and bats, as well as among larynx echolocating bats and odontocetes, reinforcing the importance of this gene to echolocation evolution. Our results contribute with previous studies using the TMC1 gene^{1, 2}. We also conducted selection analyses to

elucidate the molecular evolution of these genes between marine and freshwater odontocetes.

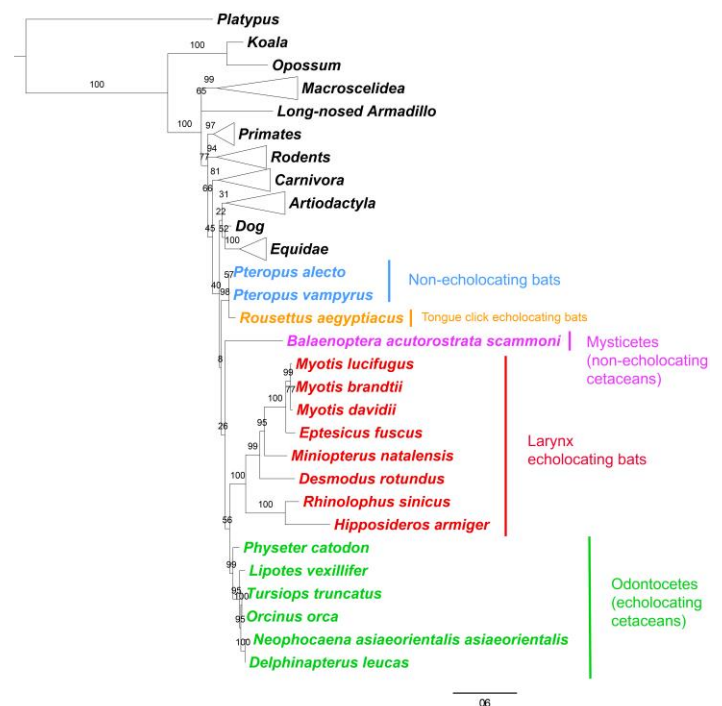


Image 1. Consensus tree of TMC1 gene for protein alignment. Author: Letícia M. M. Estevão.

Conclusions

The results indicate that TMC1 gene is an important element in the evolution of echolocation at a molecular level. Further investigation on other genes will improve our understanding of the molecular mechanisms of echolocation and also about convergent evolution.

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