



# Phylogenetic relationships of twenty *Gymnothorax* species based on cytochrome *b* sequence data

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Genet. Mol. Res. 15 (2): gmr.15028157

Received November 26, 2015

Accepted January 18, 2016

Published May 20, 2016

DOI <http://dx.doi.org/10.4238/gmr.15028157>

**ABSTRACT.** To study the phylogenetic relationships of the genus *Gymnothorax* (moray eels) distributed in South China Sea, polymerase chain reactions were performed, and the amplification products were sequenced by cloning into the PMD18T-vector (TaKaRa). The entire gene sequences encoding cytochrome *b* (1140 bp) for 16 *Gymnothorax* (*G. flavimarginatus*, *G. meleagris*, *G. undulates*, *G. reticularis*, *G. reevesi*, *G. melanospilus*, *G. rueppelliae*, *G. javanicus*, *G. chilospilus*, *G. pseudothyrsoides*, *G. fimbriatus*, *G. hepaticus*, *G. berndti*, *G. curostus*, *G. favagineus*, and *G. margaritophorus*) were obtained. Four additional *Gymnothorax* sequences from GenBank were also included. The nucleotide composition, genetic distances, and base substitution saturation analysis were calculated using the MEGA 5.0 Software. Phylogenetic analysis was performed using maximum-parsimony, maximum-likelihood (ML), and neighbor-joining (NJ). The results were as follows: 1) base-substitution saturation analysis suggested that both in third codon positions, and the full-length cytochrome *b* data

set, Ts are not saturated, but Tv substitutions may be saturated, 2) the genus *Gymnothorax*, native to the South China Sea, is divided into four distinct clades, with two clades in the NJ and ML trees, and 3) according to our experimental data, *G. melanospilus* (Bleeker, 1855) and *G. favagineus* (Bloch and Schneider, 1801) are the same species.

**Key words:** *Gymnothorax*; Mitochondrial DNA; Cytochrome *b*; Phylogenetic relationship