



<http://dx.doi.org/10.11646/zootaxa.3972.3.5>

<http://zoobank.org/urn:lsid:zoobank.org:pub:6358B61E-9A1A-4777-8391-94E90DEA19CD>

Characterization of mitochondrial control region in Merlucciidae: sequence variation and molecular phylogeny

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Abstract

In order to describe the structure and evolution of Merlucciidae and related Gadiformes mitochondrial control region we analysed 470 bp of 31 taxa belonging to 28 different species. The general structure and conserved sequence blocks observed in Gadiformes mitochondrial control region are similar to those present in other teleost fishes. The length of this segment is variable among related species due to the presence of numerous indels at domain I. Domain II is the most conserved region with a high G content. The GTGGG-box is absent in all *Merluccius* and seven other Gadidae species. Several methods of phylogenetic analyses has revealed the monophyly of Gadiformes, Gadinae and Merlucciidae. Merlucciidae is most closely related to Gadidae. Within Merlucciidae, American and Euroafrican clades show similar levels of differentiation to those within Gadinae where *Trisopterus* and *Micromesistius* are sister taxa. Genetic distance values for *Merluccius* subspecies pairs are less than half of those between species, comparable to intra specific differentiation levels in marine fish species.

Key words: Gadiformes, mtDNA control region, Genetic distance, Phylogenetic relationships

Introduction

Mitochondrial DNA has been widely used as a marker for evolutionary studies in animals due to several characteristics, including compact gene packing, lack of recombination, nearly complete maternal inheritance, faster evolutionary rate than nuclear genes and multiple copies in a cell (Pereira, 2000). In vertebrates, the mitochondrial genome contains 37 genes spread along the circular molecule and a single large non-coding region usually called control region. Variation in size of the control region is largely responsible for size variation of mtDNA. The control region is located between the genes for tRNA Proline and tRNA Phenylalanine in most vertebrate species studied (Pereira *et al.*, 2004) and contains the promoters for the transcription (LSP, HSPs), heavy-strand replication origin (O_H), and the displacement loop (D-loop). In addition, the control region generates both long-noncoding RNAs and small RNAs with regulatory potential (Jørgensen *et al.*, 2014). Based on the distribution of the variable nucleotide positions and differential frequencies of the nucleotides, it is divided into three domains (Figure S1). Most of the internal variability is located in domains I and III, which show both a high number of nucleotide substitutions and variation in length compared to domain II (Brown *et al.*, 1986; Saccone *et al.*, 1991). Conserved sequence motifs have been localized in all three domains, and some of these sequences seem to be involved in the regulation of replication and transcription (Lee *et al.*, 1995; Sbizá *et al.*, 1997). The number and location of the motifs, the spacing between them, and the degree of sequence conservation within the motifs vary considerably among and within vertebrate classes (Pereira *et al.*, 2004), suggesting that the mechanisms of regulation may differ among vertebrate orders or may involve specific nuclear-mitochondrial coevolutionary processes (Sbisá *et al.*, 1997).

Traditionally, the classification and taxonomy of Gadiformes has been based on morphological and meristic characters (Nelson, 1994 and references therein). Character polarity and homoplasy have proven to be problematic in resolving the relationships among Gadiformes taxa (Dunn, 1989). However, molecular techniques have been