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Taxonomic study of Bathygadidae fishes (Gadiformes) from Atlantic Spanish waters combining morphological and molecular approaches

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Abstract

From 2009 to 2011 eleven specimens belonging to four bathygadid species of the family Bathygadidae were captured in two different locations in the northern waters of Spain. The morphometric measurements and meristic characters of these specimens are given. The specimens were identified as belonging to the genera *Gadomus* Regan, 1903, and *Bathygadus* Günther, 1878, including the following species: *Gadomus dispar* (Vaillant, 1888), *Gadomus longifilis* (Goode & Bean, 1885), *Gadomus arcuatus* (Goode & Bean, 1886) and *Bathygadus melanobranchus* Vaillant, 1888. As a result, a new northern limit of distribution of *G. arcuatus* from the northeastern Atlantic is reported. The first molecular identification and genetic interrelationships of Bathygadidae species, based on the mitochondrial COI nucleotide sequences -DNA barcodes- is reported. Sequences corresponding to specimens from the same species were identical and the overall mean genetic diversity (uncorrected p-distance) was 0.096 ± 0.008. Based on a morphological and meristic examination of the specimens, as well as on the available literature, an updated key of the members of the family Bathygadidae from the north-eastern Atlantic Ocean is provided.

Key words: taxonomy, DNA barcoding, COI, distribution, Galicia Bank, Avilés Canyon

Resumen

Once ejemplares de cuatro especies de batigádidos pertenecientes a la familia Bathygadidae fueron capturados en dos localidades diferentes del norte de España entre los años 2009 y 2011. Se aportan sus medidas morfométricas y caracteres merísticos. Los ejemplares pertenecen a los géneros *Gadomus* Regan, 1903 y *Bathygadus* Günther, 1878, incluyendo las siguientes especies: *Gadomus dispar* (Vaillant, 1888), *Gadomus longifilis* (Goode & Bean, 1885), *Gadomus arcuatus* (Goode & Bean, 1886) y *Bathygadus melanobranchus* Vaillant, 1888. Como resultado de este estudio, se establece un nuevo límite norte de distribución de *G. arcuatus* en el Atlántico noreste. Se trata de la primera identificación molecular y exploración de las relaciones genéticas de especies de la familia Bathygadidae, basadas en las secuencias de nucleótidos del gen mitocondrial COI (código de barras de ADN). Las secuencias correspondientes a los ejemplares de las mismas especies fueron idénticas, mientras que la diversidad genética global media (distancia p) fue de 0.096 ± 0.008. Se proporciona una clave actualizada de los miembros de la familia Bathygadidae del océano Atlántico nororiental basándose en el examen de la morfología y merística de los ejemplares capturados, así como en la literatura publicada.

Palabras clave: taxonomía, ADN código de barras, COI, distribución, Banco de Galicia, Cañón de Avilés

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difficult to count, they exceeded 50 in each count (about 58 in a specimen of 292 mm TL). The number of pyloric caeca increases with the size (Howes & Crimmen, 1990), which could be the main origin of the intraspecific differences reported in literature.

Despite the fact that most of the specimens had been caught in different locations, the COI sequences from the six *G. dispar,* the three *G. longifilis* and the two *G. arcuatus* are identical and represent a single barcode each. The zero value of the intra-specific divergence in the *Gadomus* species may indicate that the COI gene appears to be conserved in this genus, but this aspect should be proved in future researches.

The bootstrap values of the ML phylogenetic tree support the formed clades, validating the haplotype sequences as barcodes for the six species investigated. Following the established procedure (Ward *et al*. 2009), it is provided for the first time a barcode sequence for the species *G. dispar*, derived from six voucher specimens that yield a single haplotype. The presence of various bathygadid sequences deposited in BOLD Databases probably resembles other scientists initiatives related to the barcoding of this or a similar group of species and will be reflected in the inclusion of these sequences in future research papers. Although only 6 out of 26 (20.7 %) bathygadid species are involved, this is the first approach to the genetic interrelationships into the family Bathygadidae.

The 'Integrative taxonomy' is defined as the science that aims to delimit the units of life's diversity from multiple and complementary perspectives (Dayrat, 2005). The DNA barcoding technique has been successfully integrated with traditional morphological analysis in the systematic studies of fishes (Baldwin & Weigt, 2012; Bañón *et al*. 2013). Taxonomic studies including morphological and molecular data could help to resolve identification mistakes and incongruities between DNA and morphological results. Molecular tools have the potential to complement taxonomic investigations by helping to reveal cryptic species, the identification of immature specimens, and the clarification of problems of synonymy (Pires & Marinoni, 2010). On the other hand, morphological analyses should be necessary to prove the correct identification of all DNA barcoded species. Errors in identification are the primary source of inaccuracies in FISH-BOL barcode data (Becker *et al*. 2011). Without verified reference sequences from voucher specimens that have been authenticated by qualified taxonomists, there is no reliable library for newly generated query sequences to be compared with (Taylor & Harris, 2012).

There were no incongruities among morphological and molecular identification in this study of the family Bathygadidae. The taxonomic identification supported the genetic analysis and viceversa, which reinforces the resulting taxonomic identification.

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