First record of the cubera snapper, Lutjanus cyanopterus (Actinopterygii: Perciformes: Lutjanidae...
FIRST RECORD OF THE CUBERA SNAPPER, *LUTJANUS CYANOPTERUS* (ACTINOPTERYGII: PERCIFORMES: LUTJANIDAE), FROM THE AZORES (NE ATLANTIC) AND POSSIBLE RANGE EXTENSION FOR THE EAST ATLANTIC

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**Background.** A lutjanid recently captured in Flores Island represents the first documented record of a snapper for the Azores Islands. Since this specimen was not made available to us besides photographs and a muscle sample, a genetic study approach was necessary in order to accurately describe and discuss this somewhat unexpected occurrence. The main objective of this paper was to explain and discuss the presence of this single specimen in this part of the north-eastern Atlantic.

**Materials and methods.** The specimen was caught by spear fishers on 30 July 2014 off Flores Island. We analysed all available photographs and a sample of muscle tissue that was taken and preserved frozen to be used for DNA barcoding.

**Results.** The specimen was a reproductively mature female with a total length of 108.7 cm and weighing 14.84 kg. The body depth of the specimen from the Azores was 2.9 in SL and the analyses conducted showed no divergence from the Canary Islands specimen reported by García-Mederos and Tuset (2014) as *Lutjanus dentatus* (Duméril, 1861) with the body depth of 2.5 in SL, which demonstrates that this character is highly variable and not useful for species identification.

**Conclusions.** The snapper specimen from the Island of Flores is a *Lutjanus cyanopterus* (Cuvier, 1828) and confirmed as first record for this part of the north-eastern Atlantic. Comparisons with a *L. dentatus* from the Canary Islands point towards synonymy although the available molecular evidence is too scarce and by no means conclusive.

**Keywords:** new record, species distribution, DNA barcoding, Macaronesia

INTRODUCTION

The snapper family Lutjanidae comprises a total of 17 genera (Nelson 2006) and approximately 110 species inhabiting tropical and subtropical coastal waters worldwide (Eschmeyer and Fong 2017, Froese and Pauly 2017). At least 17 species of the genus *Lutjanus* are known to occur in the Atlantic. There has been so far no evidence of amphi-Atlantic distribution for any of these, with 12 species recorded in the western Atlantic between Nova Scotia and south-eastern Brazil (Moura and Lindeman 2007), and five off the tropical and subtropical eastern Atlantic coast (Allen 1985). Among these, rare occurrences of the Gorcean snapper, *Lutjanus goreensis* (Valenciennes, 1830) (see González and Santana 1986, Brito et al. 2005) and the African brown snapper, *Lutjanus dentatus* (Duméril, 1861) (see García-Mederos and Tuset...
2014), in the Canary Islands, and *L. goreensis* in Madeira (Wirtz et al. 2008) have been reported, but no *Lutjanus* species was previously known from the Azores. Here we report the first record of a lutjanid snapper in the Azores archipelago, extending the previously known geographical distribution of this family to the North-eastern Atlantic.

**MATERIAL AND METHODS**

The specimen was caught by spear fishers on 30 July 2014 off the coast of Fajã Grande, Flores Island, Azores (39°27′N, 31°16′W), at around 10 m depth (Fig. 1). Morphological identification was based on photographs and using the key for Lutjanidae provided by FAO (Allen 1985). A sample of muscle tissue was taken and preserved frozen to be used for DNA barcoding.

A sample was also obtained from a specimen originally identified as *Lutjanus dentatus* (Fig. 2) that was recently caught in the Canary Islands (García-Mederos and Tuset 2014) to investigate if both specimens belonged to the same or different species.

Genomic DNA was extracted using the Jetquick Tissue DNA Spin Kit (Genomed) following the manufacturer’s protocol. A fragment of the mitochondrial cytochrome c oxidase I gene (COI) was PCR amplified using primers FishF1 and FishR1 and protocols published by Ward et al. (2005). PCR products were purified using the PureLink PCR Purification Kit (Invitrogen), then forward and reverse-sequenced on an ABI 3730xl platform at Beckman Coulter Genomics (UK). Forward and reverse sequences were edited, assembled and trimmed to a final length of 677bp using CodonCode Aligner 6.0.2 (CodonCode Corporation, Centerville, MA, USA). Consensus sequences of the two specimens were queried against the Barcode of Life Data System database (BOLD) (Ratnasingham and Hebert 2007) in order to obtain a species-level identification based on high sequence similarity. A neighbor-joining phenogram based on the Kimura 2-parameter distance model was produced using the tree-based identification tool in BOLD, to provide a graphical representation of the placement of COI sequences in relation to reference sequences of Lutjanidae.

**RESULTS AND DISCUSSION**

The fish specimen from the Azores was a female presenting mature oocytes with a total length of 108.7 cm and weighing 14.84 kg. Since we did not examine this specimen ourselves the description of the oocytes is from the catchers themselves. Although they obviously mentioned the presence of mature oocytes it is very risky to state in what precise stage they were. We have no photos of the oocytes although the most probable is that they were vitellogenic. From the examination of morphological characters according to Allen (1985), the specimen fitted the description of two species inhabit

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**Fig. 1.** The specimen of *Lutjanus cyanopterus* caught off Flores Island West coast, Azores (NE Atlantic); photo by Sílvio Gonçalves

**Fig. 2.** Non-native specimen of *Lutjanus dentatus* collected in the Canary Islands and discussed in García-Mederos and Tuset (2014); photo by Antonio García-Mederos
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Fig. 3. BOLD neighbor-joining tree based on K2P distances of public COI DNA barcodes from Lutjanidae; unknown specimen refers to the haplotype obtained for both specimens sequenced in this study.
long distance, the complete identity of COI sequences from the Azores and the Canaries, together with a slight divergence from western Atlantic ones, suggests that the source population may be located in the east Atlantic. The available molecular evidence is, however, too scarce and by no means conclusive. A comparison of genetic variation between populations from both sides of the Atlantic using high-resolution markers would help clarify this issue.

ACKNOWLEDGMENTS

We are grateful to Pedro Lima and Silvio Gonçalves who collected the specimen and kindly gave us all information possible as well as several photos. PAR was supported by an FCT post-doctoral grant (ref. SFRH/BPD/69232/2010). GC was supported by an FRCT Doctoral Grant (ref. M3.1.2/F/056/2011).

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Received: 21 April 2017
Accepted: 17 July 2017
Published electronically: 30 September 2017