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Short Communication

First record and DNA barcode for *Ocyurus chrysurus* (Lutjanidae) from a coastal lagoon in the southwestern Gulf of Mexico

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ABSTRACT. A single sub-adult specimen of yellowtail snapper, *Ocyurus chrysurus* (Bloch, 1791) of 76.08 mm total long (TL) and weighing 4.38 g, was caught on June 7, 2013 over a sandy habitat in the coastal lagoon of La Mancha, Veracruz, Mexico. The capture of *O. chrysurus* represents a first record for the lagoon and one of the few records for the estuarine systems of the southwestern Gulf of Mexico, even though this species is typical of habitats associated with coral reefs. Similarly, the reported sequence of the mitochondrial COI gene is also the first record of the species for coastal lagoons of this region. Other sequences of the same species were used to evaluate the haplotypic diversity in the western Atlantic Ocean.

Keywords: *Ocyurus chrysurus*; unusual record; genetic homogeneity; migration; coastal currents; GenBank database; environmental conditions

The Lutjanidae family includes about 113 species (Nelson *et al*., 2016), of which 14 are recognized for the southwestern Gulf of Mexico (Anderson, 2002; McEachran & Fechhelm, 2005; McEachran, 2009). One of them, the yellowtail snapper, *Ocyurus chrysurus* (Bloch, 1791) is one of the most common reef fishes in the tropical Western Atlantic Ocean (WAO), which is of great importance for commercial and artisanal fisheries (Allen, 1985; Lindeman *et al*., 2016). This species is distributed in the western Atlantic from Massachusetts south along the USA coast, Bermuda, the Bahamas, throughout the Gulf of Mexico and the Caribbean Sea, and along the South American coast to São Paulo, Brazil. Its depth range is one to 165 m, usually less than 70 m (Anderson, 2002). Adults of this species are associated with corals, while for young individuals, the seagrass beds are the most important nursery habitat. With growth, individuals move to shallow coral reef areas (McEachran & Fechhelm, 2005; Lindeman *et al*., 2016).

La Mancha Lagoon is located in the Veracruz State of Mexico (19°33’55”,19°35’44”N and 96°22’41”, 96°23’39”W) in the southwestern Gulf of Mexico (Fig. 1). It is a small lagoon with a surface of 1.58 km^2. At its northeastern end, this lagoon is connected to the sea via an inlet that discharges through a sand barrier. Thus, the aims of the present study were: 1) to report the first record of *O. chrysurus* in La Mancha Lagoon, and 2) to report the first sequence of the mitochondrial COI gene for the southwestern region of the Gulf of Mexico.

During the study of the fish community of the coastal lagoon of La Mancha (Veracruz, Mexico), 24 h sampling cycles were carried out every month from April 2012 to October 2013. Fish were collected every 2 h during each 24 h cycle, using a beach seine net (37 m long, 1.2 m deep and 1 cm mesh size). Immediately after their capture, fishes were anesthetized and posteriorly were fixed with 10% formalin and preserved with 70% ethanol. All biological collections were authorized and approved by the Cooperativa Pesquera La Mancha (fishermen’s cooperative). In particular, *O. chrysurus* is not endangered or protected in Mexico, so it was not necessary to apply for any other license (SEMARNAT, 2010).

On June 7, 2013 at dawn (06:08 h), a sub-adult specimen of yellowtail snapper, *Ocyurus chrysurus*, of 63.0 mm (standard length (SL) (76.08 mm total length (TL), weighing 4.38 g (Fig. 2), was captured at a depth

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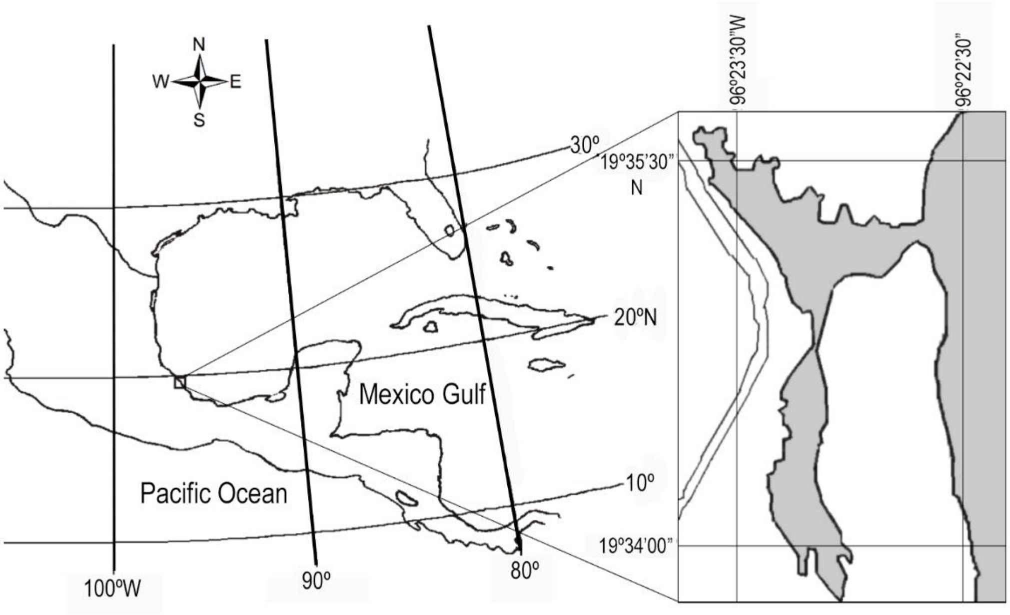

Figure 1. The geographic location of La Mancha Lagoon, Veracruz.

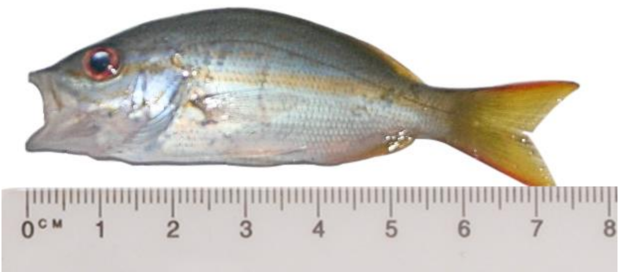

Figure 2. Yellowtail snapper, *Ocyurus chrysurus* (total length = 76.08 mm), captured on June 7, 2013 in the coastal of La Mancha Lagoon (Veracruz, Mexico).

of 1.2 m over a sandy habitat inside the lagoon (19°35'21"N, 96°22'51"W), approximately 300 m from the system inlet. This specimen was captured at 27.1°C of temperature, 37 of salinity, and 4.0 mg L^{-1} of dissolved oxygen. Measurements, counts, and color pattern of the specimen agree with those described by Allen (1985), Anderson (2002), and McEachran & Fechhelm (2005).

Tissue samples collected from caudal fin were preserved in molecular grade 95% ethanol to validate the identity of the species. DNA was obtained with a salt extraction protocol (Lopera-Barrero *et al*., 2008). Partial sequence of the barcode region of the cytochrome c oxidase subunit 1 (COI) mitochondrial gene was amplified using 25 µL reactions containing: 12.5 µL of Go *Taq* Green Master Mix (PROMEGA), 0.3 µL of MgCl$_2$ (25nM), 1.0 µL of each primer (10 µM), 9.2 µL of double distilled water and 1.0 µL of template DNA (50 ng µL^{-1}). Primers used were universal: FishF1 (5'-TCAACCAACCACAAAGACATTGGCAC-3') and FishR1 (5'-TAGACTTCTGGGTGGCCAAAG AATCA-3') (Ward *et al*., 2005). PCR cycling parameters consisted of denaturation of 2 min at 94°C, followed by 35 cycles of 30 s at 94°C, 40 s at 52°C and 1 min at 72°C, and a final elongation of 10 min at 72°C. The sequencing was carried out using the Big-Dye Terminator v3.1 Sequencing kit (Applied Biosystems, USA). After the cycle sequencing reactions, unincorporated dye terminators were removed with Centrisep spin columns (Princeton Separations, Inc.). The sequencing reaction product was run on an ABI Prism 3130XL capillary sequencer (Applied Biosystems). The sequence electropherogram was edited in MEGA-X and was compared with the database of BOLD Systems.

Additional COI sequences (40) were downloaded from the GenBank database to evaluate if exists a relationship of the captured organism with other specimens distributed along the WAO. These sequences, according to 10 geographical localities, are Alabama, USA (KF461208); Florida, USA (JQ841941); Bahamas (JN021311, JQ839852, JQ839853, JQ839854); Quintana Roo, México (GU224995); Belize (GU225407, GU225408, GU225409, GU225410, GU225411, KF930198, JQ840190, JQ840191, JQ840192, JQ840193); Virgin Islands, USA (FJ998487, FJ998488, GU224985, GU224986, GU224987, GU224988, GU224989, GU224990, GU224991, GU224992, GU224993, GU224994); Curazao (JQ842255, JQ842256, JQ842257); Panama (FJ998489); Tobago Island (JQ842973); São Paulo,

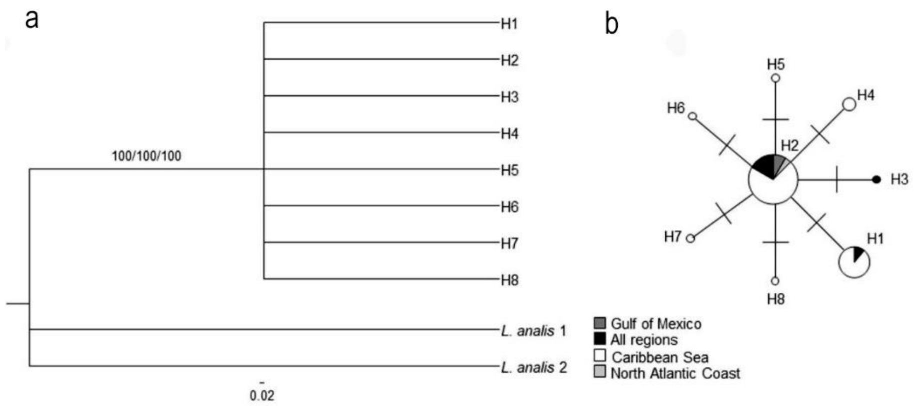

Figure 3. a) Bayesian, maximum-likelihood and neighbor-joining tree of the haplotypes identified for *Ocyurus chrysurus* (respective support values are shown at the nodes), with the partial sequences of the mtDNA COI gene, obtained from localities throughout Western Atlantic Ocean (WAO). H1: Bahamas, Quintana Roo, Belize, Virgin Islands, and São Paulo; H2: Alabama, Florida, Bahamas, Veracruz (present record), Belize, Panama, Virgin Islands, Curacao, Tobago, and Sao Paulo; H3: São Paulo; H4: Virgin Islands; H5: Virgin Islands; H6: Virgin Islands; H7: Virgin Islands; and H8: Bahamas. Outgroups correspond to *Lutjanus analis*, b) haplotype network inferred, short lines between haplotypes indicate the number of mutations occurred, and the size of circles represent the frequency of each haplotype.

Brazil (JQ365458, JQ365459, JQ365460, JQ365461, JQ365462, JQ365463); for a total of 40 sequences. According to genetic distances among lutjanid species (Chu *et al*., 2013; Veneza *et al*., 2014), the nearby species *Lutjanus analis* was used as an outgroup using two sequences (HQ987863, GU225352). The sequences were aligned using MEGA-X (Kumar *et al*., 2018). The haplotypes, haplotypic diversity and phylogenetic estimations were produced by Bayesian inference (BI), with five Markov chains, 10,000,000 generations and discarding 25% of burn-in using Mr. Bayes v.3.2 (Ronquist *et al*., 2012); maximum-likelihood (ML) and neighbor-joining (NJ) methods were estimated with PAUP v. 4.0b10 software (Swofford, 2002) with 1000 replicates of Bootstrap (Felsenstein, 1985). The best evolutionary method was TPM3uf+1 estimated by jModeltest v.2.1.6 using Akaike's information criteria (Posada, 2008). A haplotype network was estimated using Networks v. 4.6.1.3 (Bandelt *et al*., 1999) to infer the genealogical relationships between haplotypes to calculate the genetic distances among haplotypes, pair-wise genetic distance values (K2P) based on COI sequences were estimated using MEGA-X.

The partial sequence of the mitochondrial COI gene produced 604 nucleotide base pairs. The comparison with the BOLD Systems database showed a probability of placement of 100% of this sequence with the species *Ocyurus chrysurus*. This sequence data has been submitted to the GenBank database under accession number KU314764.

Regarding the haplotype analysis, the 41 sequences of *O. chrysurus* were grouped randomly (without any geographical arrangement) into eight different haplotypes. The sequence of the present specimen was grouped into the haplotype with a greater number of sequences (H2 with 25 sequences), which included at least one sequence from nine of the 10 geographical localities considered. Considering the wide latitudinal distribution of the sequences (from Alabama to Brazil), the high similarity between the haplotypes (with genetic distances from 0.0016 to 0.0032) indicates the lack of genetic structure between these locations. The haplotype network also shows little genetic variation between haplotypes, with signals of population expansion (Fig. 3).

The capture of *O. chrysurus* represents a first record for the La Mancha Lagoon and one of the few records for estuarine systems in the southwestern Gulf of Mexico (Froese & Pauly, 2019; GBIF, 2019), even though this species has been widely reported as restricted to coral reefs environments.

According to Ortiz-Lozano *et al*. (2013), the coral formations closest to La Mancha Lagoon is Punta Gorda (43 km). Thus, the catch of the specimen reported here could have been originated by a migration from the closest reefs reported. This migration could have been facilitated by following the northwestward currents predominant from May to August on the Veracruz coasts (Allende-Arandía *et al*., 2016), despite the fact that the acoustic tracking of five individuals of *O. chrysurus* near the marine reserves in Dry Tortugas, Florida, estimated an average home range of about 4.17

± 1.75 km^2, with a maximum value of 10.72 km^2 (Farmer & Ault, 2011).

According to the GenBank and BOLD Systems databases, the reported sequence of the mitochondrial COI gene is also the first record for the species in the southwestern region of the Gulf of Mexico. The results obtained about the haplotypic diversity analysis seem to indicate that the specimens of *O. chrysurus* distributed along the WAO (from Alabama to Brazil) are genetically homogeneous, without any genetic structure, at least to the mitochondrial COI gene. In this way, the pattern of genetic homogeneity observed in *O. chrysurus* in the present study is similar to that found in other lutjanids (Da Silva *et al*., 2015). Even other studies that use molecular markers with a higher evolutionary rate (nuclear microsatellites and others mtDNA sequences) have provided evidence of significant, although weak genetic differences among different geographic samples of *O. chrysurus* (Saillant *et al*., 2012).

Studies that also use molecular markers with a high rate of change (cytochrome b and mtDNA control-region) showed no differences among *O. chrysurus* populations distributed along more than 3,000 km of the Brazilian coast (Vasconcellos *et al*., 2008; Da Silva *et al*., 2015). Although, these studies have also suggested restriction of gene flow between Belize (Caribbean) and Brazilian localities, the absence of sampled individuals between these two regions made it difficult to conduct more analyses on historical connectivity between populations in this geographic range (Da Silva *et al*., 2015). By contrast, in the present study, 32 sequences corresponding to seven localities in the Caribbean were considered (from the Bahamas to Panama and Tobago), including a southernmost record in Brazil (São Paulo).

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