

## Marine Record

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### Corresponding author:


Juan Carlos Arronte;

Email: [jcarlos.arronte@ieo.csic.es](mailto:jcarlos.arronte@ieo.csic.es)

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# First record of *Diapterus brevirostris* (Teleostei: Gerreidae) in Atlantic European waters: a case of introduced species

Juan Carlos Arronte<sup>1</sup> , Ana Antolínez<sup>1</sup>, Rafael Bañón<sup>2</sup>, José Heredia<sup>3</sup> and Alejandro de Carlos<sup>4,5</sup>

<sup>1</sup>Instituto Español de Oceanografía (IEO- CSIC), C.O. de Santander, Santander, Spain; <sup>2</sup>Grupo de Estudio do Medio Mariño (GEMM), Ribeira, Spain; <sup>3</sup>Servicio de Ordenación Pesquera, Dirección General de Pesca Marítima, Consejería de Medio Rural y Cohesión Territorial, Gijón, Spain; <sup>4</sup>Departamento de Bioquímica, Xenética e Inmunoloxía. Facultade de Bioloxía, Universidade de Vigo, Vigo, Spain and <sup>5</sup>Centro de Investigación Mariña, Universidade de Vigo, Vigo, Spain

## Abstract

*Diapterus brevirostris* (Sauvage, 1879) is a fish of the family Gerreidae, native to the tropical and subtropical waters of the Pacific coast of America. A specimen of this species was captured off the coast of Asturias, Spain. To the best of our knowledge, this is the first record of the genus *Diapterus* in the North Atlantic. Given its small size (6.4 cm), it is likely that the species was present in the area for a relatively short time. Although the introduction pathway is unknown, the species' native area and the proximity of a major port to the site of capture suggest that ship's ballast water is the most likely vector of introduction.

## Introduction

In the marine context, the introduction and spread of non-native species (NIS) is not only considered to be one of the major threats to biodiversity and ecosystem functioning, but also responsible for changes in the biota and economic losses in some fisheries (Katsanevakis *et al.*, 2014; Öztürk, 2021). According to Falk-Petersen *et al.* (2006), the term introduction can be defined as the direct or indirect movement of an organism by human activities beyond the limits of its native geographical range into an area where it does not occur naturally. However, the terminology associated with introduced species is evolving, and terms such as acclimatised, adventive, naturalised, or immigrant species are now considered to be a subset of introduced species.

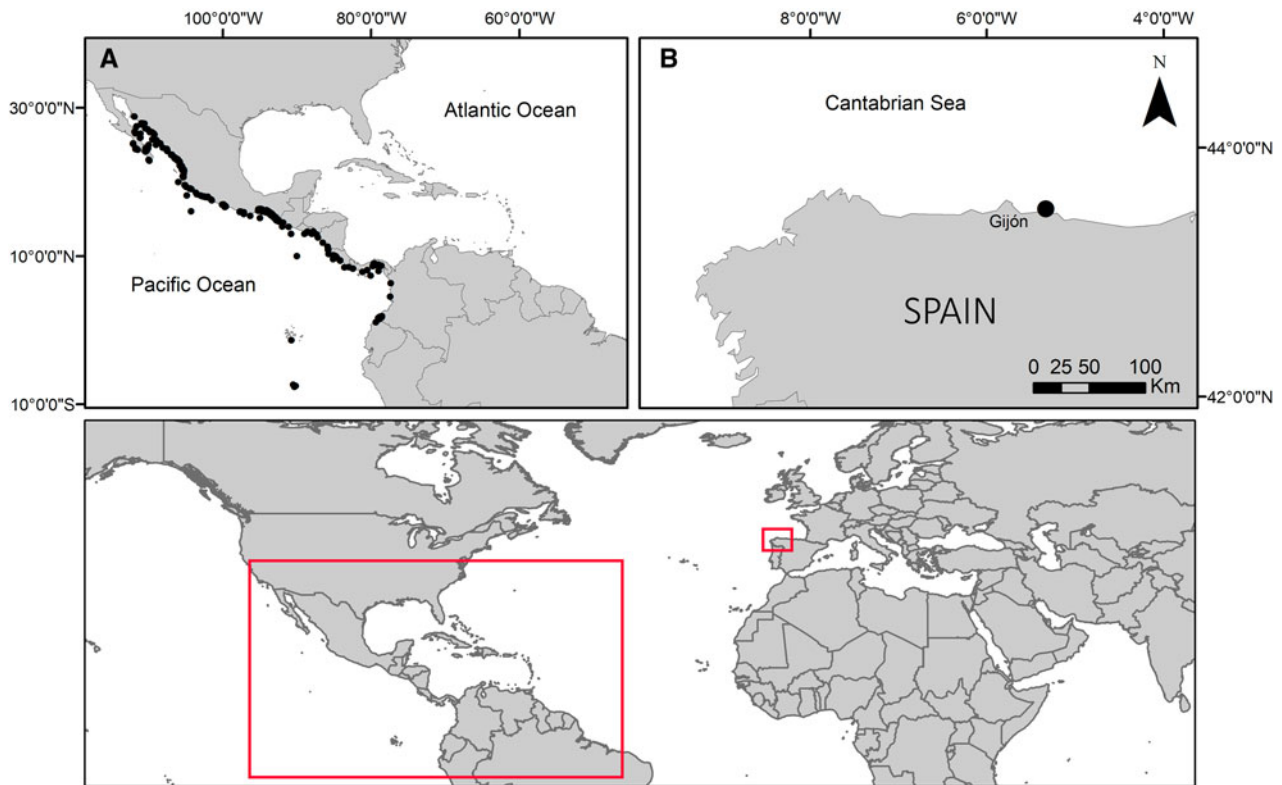
The genus *Diapterus* Ranzani 1842 is one of the seven genera that make up the Family Gerreidae, commonly known as mojarras (Fricke *et al.*, 2024). The taxonomy of the Gerreidae is confusing and the subject of debate within the scientific community (e.g. Chen *et al.*, 2007; González-Acosta *et al.*, 2007; De La Cruz-Agüero *et al.*, 2012; Chollet-Villalpando *et al.*, 2024). *Diapterus* has also been affected by these taxonomic uncertainties and, with the establishment of the validity of the short nose mojarras *Diapterus brevirostris* over the Peruvian mojarras *D. peruvianus* (González-Acosta *et al.*, 2007), and the separation of *D. aureolus* from the genus (Vergara-Solana *et al.*, 2014), the genus currently comprises three species distributed throughout the tropical and subtropical sea coastal waters of both coasts of America: the Irish pompano *D. auratus* Ranzani 1842 and the rhombic mojarras *D. rhombeus* (Cuvier 1829) from the western Atlantic Ocean, while *D. brevirostris* (Sauvage, 1879) is distributed along the Pacific Ocean (Vergara-Solana *et al.*, 2014).

*D. brevirostris* occurs on sandy or muddy bottoms of bays, estuaries, and coastal lagoons bordered by mangroves along the tropical eastern Pacific coast from the west coast of Baja California (Bahía Magdalena, including the Gulf of California) to northern Peru (González-Acosta *et al.*, 2007 and references therein) (Figure 1a). Here we document the first record of *D. brevirostris* in the Cantabrian Sea (northeastern Atlantic) and discuss the possible pathways for its presence in this area.

## Material and methods

On 3 September 2021, a specimen of an unknown fish species was recorded from off the coast of Asturias, northern Spain (43° 33' 17N – 5° 24' 55W) (Figure 1b). The individual was collected by a recreational angler at a depth of approximately 25 m. It was regurgitated from the stomach of a captured specimen of Comber *Serranus cabrilla* (Linnaeus, 1758).

The fish was frozen and shipped to the Instituto Español de Oceanografía (IEO-CSIC) for identification and further analysis. It appeared that the individual had been digested by the *S. cabrilla* specimen shortly before its predator was captured, resulting in a slight degree of damage that allowed its morphological identification. Once in the laboratory, the specimen was identified morphologically using published identification keys and descriptions



**Figure 1.** (A) Native distribution\* of *Diapterus brevirostris* in the Pacific Ocean. (B) Location of the occurrence of *D. brevirostris* off the coast of Asturias, Spain (NE Atlantic). \*Data on the occurrence of *D. brevirostris* in the Pacific Ocean were downloaded from the Global Biodiversity Information Facility (GBIF) (GBIF, 2023).

(Castro-Aguirre *et al.*, 1999; Vergara-Solana *et al.*, 2014). The fish was weighed to the nearest 0.1 g, measured to the nearest 0.1 mm with a digital caliper and subsequently deposited in the marine collection of the Instituto Español de Oceanografía in Santander (IEO-COST ST3931).

To confirm the species identification, a sample of muscle tissue was collected and preserved in absolute ethanol for molecular DNA barcoding of the mitochondrial cytochrome oxidase I gene (*COI*). The DNA of the specimen was extracted from a muscle tissue sample using the E.Z.N.A. Tissue DNA Kit from Omega-Biotek, following the manufacturer's instructions. The region of the genome that serves as a barcode for molecular identification, COI-5P, was amplified using the universal primers LCO1490 and HCO2198 (Folmer *et al.*, 1994), following the protocol used by Hebert *et al.* (2003). The sequences of both DNA strands were obtained at the 'Centro de Apoyo Científico y Tecnológico a la Investigación' (CACTI, University of Vigo, Spain), by the Sanger chain termination method (Sanger *et al.*, 1977), using the same primers. The consensus sequence, comprising 652 nucleotides, was aligned with other sequences of the same genus. The relationships between all sequences were then represented through the construction of a Neighbour-Joining diagram (Saitou & Nei, 1987). The differences between the sequences were calculated as the ratio of distinct nucleotides to the total length without the application of any evolutionary model (uncorrected p-distance) (Nei & Kumar, 2000). To facilitate the molecular identification of the specimen captured in Asturias, sequences of the COI-5P marker of all Barcode Index Numbers (BINs) of the genus *Diapterus* were downloaded from the BOLD database.

The partial COI sequence data with all meta-data were registered on the Barcode of Life Database (BOLD Systems; [www.boldsystems.org](http://www.boldsystems.org)) as part of the project entitled 'Unusual Atlantic Fishes' (code UNAFI) with process ID UNAFI013-24

**Table 1.** Morphometric measurements in mm and as percentage of standard length (%SL) and meristic counts recorded on the specimen of *D. brevirostris* captured off Asturias, Spain (northeastern Atlantic)

Morphometric	Size (mm)	Proportion (% SL)
Total length (TL)	64.2	---
Standard length (SL)	45.6	---
Maximum body depth	21.8	47.8
Pre-orbital length	5.5	12.1
Eye diameter	5.7	12.5
Head length	17.3	37.9
Pre-dorsal length	18.0	39.5
Pre-pelvic length	18.7	41.0
Pectoral length	11.8	25.9
Peduncle depth	6.3	13.8
1st dorsal fin ray length	2.4	5.3
2nd dorsal fin ray length	7.3	16.0
1st anal fin ray length	2.2	4.8
2nd anal fin ray length	11.0	24.1
Meristic		
Dorsal fin rays	IX - 10	
Anal fin rays	III - 8	
Pelvic fin rays	I - 5	
Pectoral fin rays	Damaged	
Total body weight (gr)	2.67	



Figure 2. *Diapterus brevirostris* captured off the coast of Asturias coast (northeastern Spain).

and deposited in GenBank (<https://www.ncbi.nlm.nih.gov/genbank/>) under accession number PP789894.

Results

The specimen (Figure 2) was taxonomically attributed to the genus *Diapterus*, as evidenced by the serrated margin of the preopercle, the smooth preorbital bone, and the rhomboid body (Vergara-Solana *et al.*, 2014). The individual is consistent with the description of *D. brevirostris* by González-Acosta *et al.* (2007) and Vergara-Solana *et al.* (2014), and the COI results showed 100% similarity with records of *D. brevirostris* available in BOLD. The captured individual presented a rhomboidal and laterally compressed body, with a maximum height contained within 2.1 times the standard length. The mouth was protractile, the posterior and inferior margins of the preopercular bone were

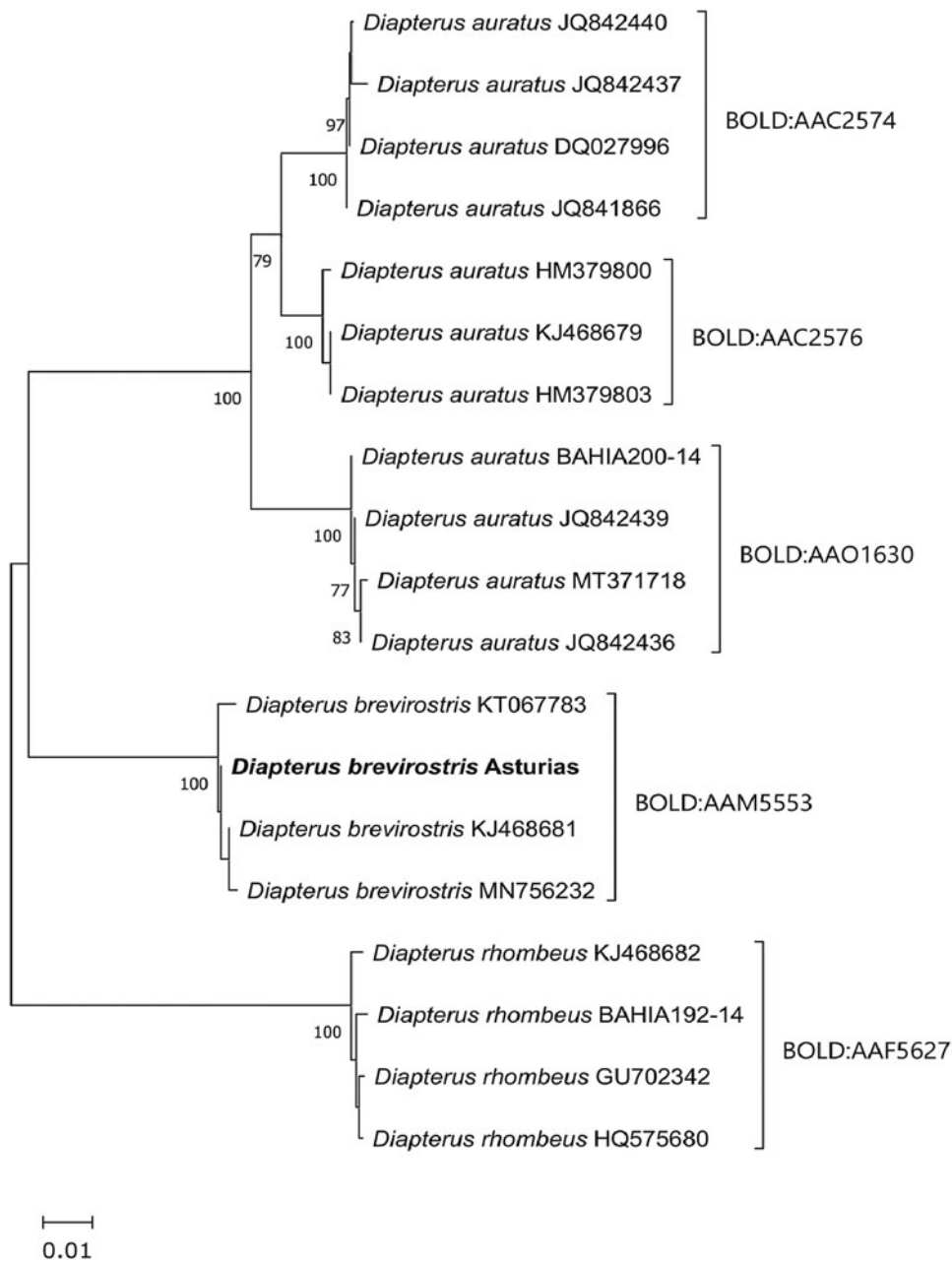


Figure 3. Neighbour-Joining (NJ) tree of COI-5P sequences from *Diapterus* specimens. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches. The tree is drawn to scale, with branch lengths in the units of the number of base differences per site (p-distance). All ambiguous positions were removed for each sequence pair (pairwise deletion option). The analysis involved 19 nucleotide sequences and 655 nucleotide positions. The *Diapterus* BIN clusters are indicated. The specimen captured off the Asturias coast (northeastern Atlantic) is in bold.

serrated, and the preorbital bone had a smooth edge. The dorsal fin was elevated at the front, with nine spines (the second being the longest) and ten soft rays. The anal fin exhibited long lobes with three spines (the second being the longest) and eight soft rays. The pectoral fins were located slightly posterior the origin of the anal fin. All the meristic and morphometric data for the specimen are presented in Table 1.

As the specimen was regurgitated, many features of its body colouration were lost. However, its body was silvery with yellowish anal and pelvic fins with blackish membranes.

The Neighbour-joining (NJ) analysis indicates that the sequence of the Asturias specimen in the BIN belongs to BOLD: AAM5553, which is comprised of sequences of *D. brevis*. The genetic distances between these sequences vary within the range 0–0.6% (Figure 3). This cluster is clearly distinguished from adjacent clusters, exhibiting distances to nearest neighbours of 9.6% with BOLD: AAO1630, formed by *D. auratus*, and 11.9% with BOLD: AAF5627, corresponding to *D. rhombeus*. A comparison of the 19 sequences used in the analysis revealed a bar-coding gap between distances of 0.66% and 2.29%. It is noteworthy that three of the BINs comprise sequences of the species *D. auratus*.

## Discussion

The present study provides evidence of the occurrence of *D. brevis* in the northeastern Atlantic, based on both morphological and molecular identification. This represents the first documented occurrence of the species outside their native habitat in the eastern Pacific Ocean and the genus in the eastern Atlantic. In this area, the family Gerreidae is represented by only two species with their distribution along the west African coasts, Flagfin mojarra *Eucinostomus melanopterus* (Bleeker, 1863) and Guinean striped mojarra *Gerres nigri* Günther, 1859 (Iwatsuki, 2016).

The presence of fish species outside their native range can occur through natural mechanisms such as ocean currents (Wolff, 2005) or through human-induced vectors such as deliberate introductions (e.g. aquaculture, sport fishing, and ecosystem management), aquarium releases, and ship ballast water (Wolff, 2005; Morais & Teodósio, 2016).

The small size (6.4 cm) and weight (less than 3 gr) of the *D. brevis* specimen, rules out the possibility that it entered the North Atlantic through the Panama Canal and then reached the northeastern coast of Spain by natural means. Consequently, the presence of the species is likely to be the result of human-mediated translocation. The species is not known to be farmed or part of the aquarium trade industry, which makes ballast water the most likely vector of introduction into the Cantabrian Sea. In addition, the specimen was captured near the major commercial port of Gijón, where not only have non-native species been previously recorded (Cabal *et al.*, 2006), but also where merchant vessels from the species' range had docked in the weeks prior to the capture (personal communication, Port Authority of Gijón). Ballast water from ships is a significant transport vector of non-native and invasive aquatic species (Gollasch *et al.*, 2002). In the eastern Atlantic, ballast water has been identified out as a mechanism for the arrival of several native fishes from the western Atlantic, including *Micropogonias undulatus* (Linnaeus, 1766) (Stevens *et al.*, 2004), *Trinectes maculatus* (Bloch & Schneider, 1801) (Wolff, 2005) and *Cynoscion regalis* (Bloch and Schneider, 1801) (Morais & Teodósio, 2016; Bañón *et al.*, 2018).

The introduction of numerous Indo-Pacific fish species through the Suez Canal (Lessepsian migration) is a well-documented phenomenon in the Mediterranean (Golani *et al.*, 2002). In European Atlantic waters, the occurrence of fish species with an

Indo-Pacific origin is very rare. Prior to the present record, only the presence of *Sebastes schlegelii* Hilgendorf, 1880 in Dutch coastal waters (Kai & Soes, 2009) and *Sebastiscus marmoratus* (Cuvier, 1829) in Norwegian waters (Hansen & Karlsbakk, 2018) have been reported. However, in contrast to these two records, our individual is less than one year old (Gallardo-Cabello *et al.*, 2014) and immature (Gallardo-Cabello *et al.*, 2015). In view of these two factors, and the exceptional occurrence of the species in the Cantabrian Sea, it is highly unlikely that an established population will be present in the area in the future.

Non-native marine fishes can have negative ecological impacts through several mechanisms, including habitat and/or food web alteration, competition, and predation on native species, vectoring of parasites and pathogens, and genetic impacts on native species (Arndt *et al.*, 2018). However, given the medium size of the species (maximum size of 38 cm TL) and its carnivorous feeding habits based mainly on benthic organisms such as copepods, ostracods, polychaetes, and molluscs (González-Acosta *et al.*, 2007), it is likely that its impact on the ecosystem would be low in the hypothetical case of establishment in the temperate north-eastern Atlantic.

In addition to reporting the first record for *D. brevis* in the eastern Atlantic, this study also highlights the importance of motivating the public to contribute to knowledge, a non-scientific tool that has proven its usefulness in detecting non-native species (Azzurro *et al.*, 2018; Encarnaçao *et al.*, 2021).

**Data.** The authors confirm that the data supporting the findings of this study are available within the article.

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**Author contributions.** AdC conducted lab work and performed the molecular analysis. AA performed morphological analyses. JH and AA contributed to manuscript preparation. The manuscript was written by JCA with significant contributions by RB and AdC. All authors commented on and approved the final version of the manuscript.

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**Competing interests.** None.

**Ethical standards.** Not applicable.

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