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Revisiting the sawback angelshark (*Squatina aculeata* Cuvier, 1829): new insights on distribution, morphology, and conservation in the Central Mediterranean Sea

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Abstract

The sawback angelshark (*Squatina aculeata* Cuvier, 1829) is a critically endangered species in the Mediterranean Sea, facing severe population decline due to overfishing and bycatch. This study provides biomolecular and morphological analyses of a specimen captured off Avola, in the eastern part of Sicily. A female individual of 144.7 cm in total length was caught at a depth of 16 m and was identified through an integrative taxonomy approach. Morphometric assessments revealed a positive allometric growth pattern ($TW = 0.1156 \bullet TL^{2.4728}$; $R^2 = 0.8913$). The sparids' remains found in the stomach confirm the feeding behavior characteristic of angelsharks. Additionally, vertebral band analysis suggested an estimated birth total length of approximately 21.8 cm. The study highlights the possible presence of breeding and nursery areas in the central Mediterranean, underlining the need for enhanced conservation efforts and developing a coordinated Mediterranean monitoring network to improve the knowledge and protection of this vulnerable species.

Keywords Integrative taxonomy · Bycatch · Length–weight relationship · Vertebral band analysis · Nursery grounds

Introduction

Chondrichthyans are widely distributed in marine ecosystems; however, over the years, they have faced a drastic decline due to overfishing, habitat loss, and bycatch globally. The Mediterranean Sea has been classified as one of the areas where shark and ray biodiversity is at greater risk (Dulvy et al. 2024), and approximately 50% of the 78 species of elasmobranchs are listed as critically endangered, endangered, or vulnerable.

Among the most imperiled are angelsharks (family Squatinidae), whose biological characteristics—such as slow growth and low fecundity—make them especially vulnerable to exploitation (Rodríguez-Cabello et al. 2008; Tiralongo et al. 2018, Dulvy et al. 2021). Despite their ecological importance as top or mesopredators, they have historically received less management attention compared to bony fishes. Their decline has led to cascading effects in marine food webs, potentially altering the structure and functioning of entire ecosystems (Heithaus et al. 2008).

Globally, this family comprises 24 recognized species (Weigmann et al. 7), with three knowns to inhabit the Mediterranean: *Squatina oculata* Bonaparte, 1840; *Squatina squatina* (Linnaeus, 1758); and *Squatina aculeata* Cuvier, 1829. These three species are among those for which capture and trade have been prohibited since 2012 under the General Fisheries Commission for the Mediterranean (GFCM)

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Recommendation GFCM/36/2012/3 (Anonymous 2016) and it is also listed in Annex II of the Barcelona Convention (UNEP/MAP-SPA/RAC 2018). Angelsharks are flat-bodied and demersal, inhabiting sandy or muddy seabeds at depths of 0–1289 m (Weigmann 2016), where they feed and take shelter (Golani et al. 2007). These characteristics make them highly susceptible to bottom-fishing practices, including trawling and fixed net (gillnets and trammel nets, as well as recreational fishing, often resulting in incidental capture (Morey et al. 2017).

Historically, *Squatina aculeata* Cuvier, 1829, also referred to as "sawback angelshark," has been reported from the Eastern Atlantic, ranging from Morocco to Angola, and across the central and western Mediterranean (Miller 2016); it was considered rare in the Eastern Mediterranean (Serena 2005). However, in the early 2000 s, few records from the coasts of Turkey, Greece, and Eastern Sicily (Italy) were reported. For instance, Başusta (2002) described a male specimen found in May 1997; Filiz et al. (2005) documented one specimen in the Gulf of Gokova, Turkey; in 2007, Corsini and Zava (2007) documented a specimen caught via trawling in the Aegean Sea, northwest of Rhodes, Greece, and additional observations have followed. These findings, among others, have prompted researchers (Miller 2016; Zava et al. 2020, 2022) to reconstruct the distribution of the species based on the literature. Nevertheless, the species is still considered rare (De Maddalena 2024). This study aims to expand current knowledge of *Squatina aculeata* by analyzing an accidental capture recorded in 2023 in Avola, off the coast of Eastern Sicily in the Central Mediterranean Sea. We present the results of biomolecular analysis and morphological data conducted on the collected specimen, along with a detailed examination of stomach contents to contribute to the limited understanding of the species' diet. Additionally, this work offers a novel contribution to age determination in this species through analysis of vertebral growth bands, providing insight into the longevity of *S. aculeata* for the first time.

Material and method

The specimen was sampled in the context of the National Fisheries Data Collection Framework (DCF), which provides for the collection and management of biological, environmental, technical, and socio-economic data necessary for fisheries management purposes (EU Regulation no. 1004/2017), during fishing activity targeting *Sepia officinalis*. Unfortunately, the specimen was found in the net, already dead, upon retrieval. Therefore, not deliberately captured for the purpose of this study.

The species was morphologically identified as *Squatina aculeata* (Compagno, 1984; Fischer, 1987) as it presented dorsal spines, heavily fringed nasal barbels and anterior nasal flaps, and the absence of ocelli (eye-spots) on its body. In the laboratory, morphometric analyses were carried out (Fig. 1). The morphological measurements were taken to the nearest millimeter. The total weight (TW), eviscerated weight (EW), liver weight (LW), and gonad weight (GW) were recorded to the nearest gram. In total, 72 morphological measures were taken (see Supplementary Materials 1 for further details). Moreover, morphological data from the literature were gathered, and additional observations were reviewed and added to the list (Supplementary Materials 1). Furthermore, based on the coordinates availability or capture site described in the literature, the species' distribution was reconstructed based on available coordinates, or capture site descriptions, and it resulted in 45 observations (Fig. 2). All capture sites, coordinates, and depth, are available in Table 2.

The relation between total weight [TW—g] and total length [TL—cm] was calculated using the equation TW = a TLb, where a is a constant depending on the species and b is the allometric parameter. Data from TW and TL were retrieved from the literature, when possible, and integrated with the present study's specimen data (Supplementary Materials 1).

The stomach was dissected and frozen at −20 °C. Afterwards, the content was analyzed and classified to the lowest taxonomic level possible. The fullness of the stomach was assessed based on a four-level scale: 1 empty, 2 < 50% filled; 3 > 50% filled; 4 bursting (Garrido et al. 2008).

A sample of about 10 vertebrae was extracted from the thoracic-predorsal region (immediately posterior to the scapular origin of the vertebral column), where the vertebral centra are bigger and thus easier to analyze (Campana 2014). Subsequently, to estimate the specimen's age, three vertebral centra were cleaned from soft tissue by scalpel and embedded in epoxy resin (Prochima E-30). Thin sections were carried out by a cutting machine, Remet Secotron 200, with a circular diamond blade (diameter, 125 mm; thickness, 0.33 mm). The sections had an initial width of 0.5 mm and were thinned to increase their readability by grinding with sandpaper (grit 800), leading to a final width of about 0.4 mm. The sections were then immersed in a clarification medium, such as seawater, and examined under a stereomicroscope with transmitted light. The corpus calcareum length (CCL) was measured, and the birthmark (BM) in the vertebral centrum was identified as the first clear mark corresponding to a change of angle in the CCL shape (Sulikowski et al. 2003; Carbonara et al. 2020a, b).

Total genomic DNA was extracted from muscle tissue preserved in 95% ethanol using the DNeasy blood and tissue kit (Qiagen) following the manufacturer's instructions.

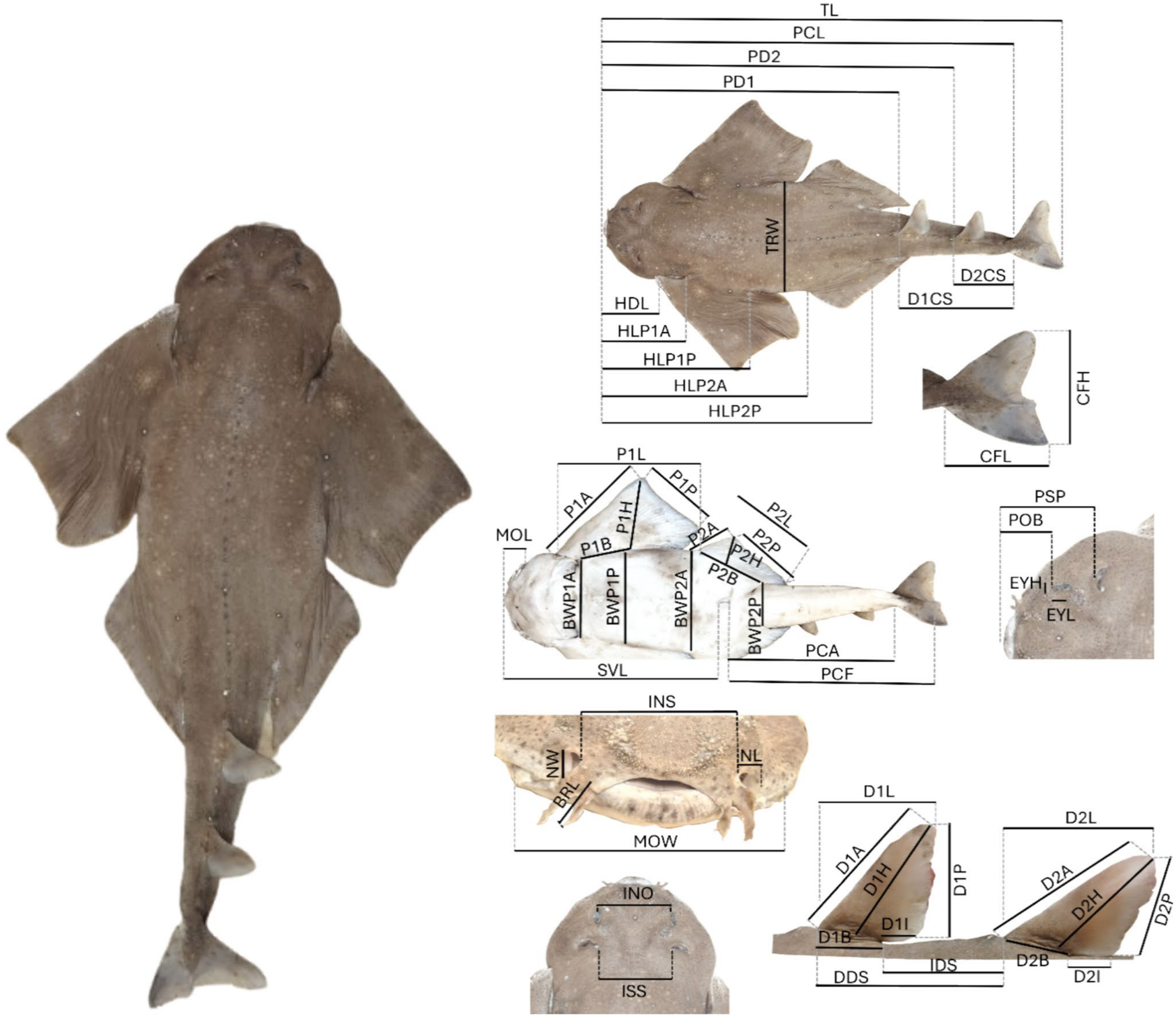


Fig. 1 Morphometric measurements carried out on *S. aculeata*. Acronyms's meaning: TL, total length; PCL, precaudal length; SVL, snout-ventral length; CFL, caudal fork length; CFH, caudal fork width; CPH, caudal peduncle height; PCA, pelvic fin caudal fin space; PCF, pelvic to caudal fork; PD1, pre-first dorsal-fin length; PD2, pre-second dorsal-fin length; D1CS, FIRST dorsal to caudal space; D2CS, second dorsal to caudal space; POB, pre-orbital length; PSP, pre-spiracle length; TRW, trunk width; HDL, head length; HDW, head width; EYH, eye height; EYL, eye length; INO, interorbital distance; NW, nostril width; NL, nostril length; INS, internarial space; ISS, distance between spiracles; MOW, mouth width; BRL, barbels length; MOL, mouth length; D1A, first dorsal fin anterior margin; D1B, first dorsal fin base; D1H, first dorsal fin height; D1L, first dorsal fin length; D1P, first dorsal fin posterior margin; D1I, first dorsal inner margin; IDS, interdorsal space; D2A, second dorsal fin anterior margin; D2B, second dorsal fin base; D2H, second dorsal fin height; D2I, second dorsal fin inner margin; D2L, second dorsal fin length; D2P, second dorsal fin posterior margin; P1A, pectoral fin anterior margin (left/right); P1B, pectoral fin base (left/right); P1H, pectoral fin height (left/right); P1L, pectoral fin length (left/right); P1P, pectoral fin posterior margin (left/right); P2A, pelvic fin anterior margin (left/right); P2B, pelvic fin base (left/right); P2H, pelvic fin height (left/right); P2L, pelvic fin posterior margin length (left/right); P2P, pelvic fin length (left/right); BWP1A, body width between armpits of pectoral anterior insertion; HLP1A, body length head to armpits of pectoral anterior insertion; BWP1P, body width between armpits of pectoral posterior insertion; HLP1P, body length head to armpits of pectoral posterior insertion; BWP2A, body width between armpits of pelvic anterior insertion; HLP2A, body length head to armpits of pelvic anterior insertion; BWP2P, body width between armpits of pelvic posterior insertion; HLP2P, body length head to armpits of pelvic posterior insertion; DDS, first to second dorsal fin space

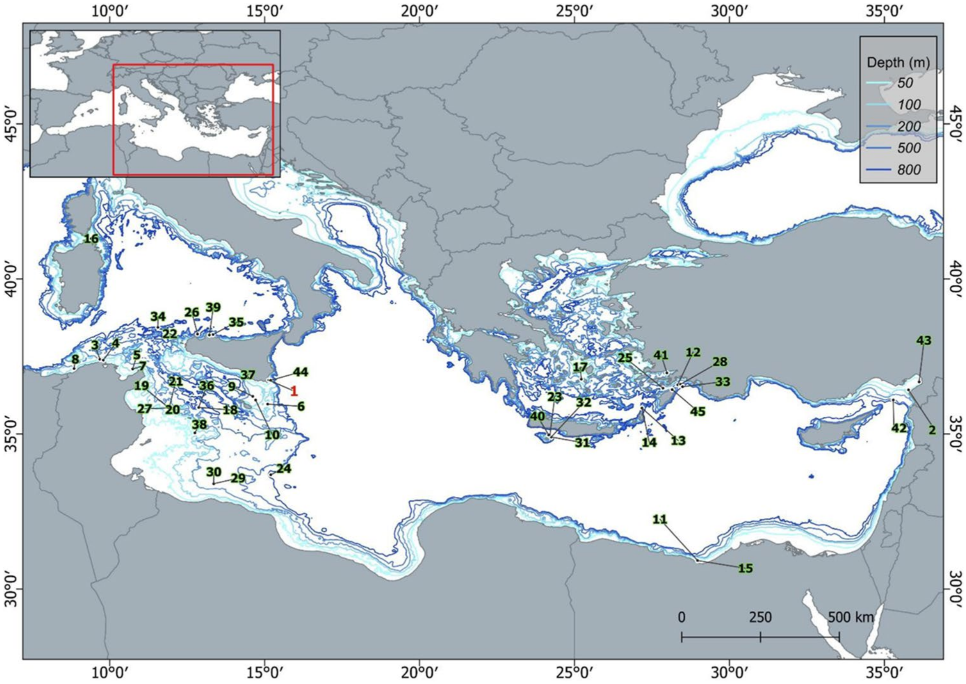


Fig. 2 Locations of 45 *Squatina aculeata* sightings reported in the central Eastern Mediterranean Sea between 1997 and 2024. The specimen discussed in this study is marked in red, whereas the black numbers correspond to the other specimens' records listed in Table 1

A partial fragment of the mitochondrial Cytochrome Oxidase subunit I (COI) gene was obtained using the primers VF2_t1- and FishR2_t1 (Ivanova et al. 2007) and the PCR amplification conditions described in Pappalardo et al. (2024). The amplified product was checked through 1% agarose gel electrophoresis and purified with the QIAquick PCR purification kit (Qiagen). Subsequently, sequencing was bidirectionally performed by Eurofins Genomics (https://eurofinsgenomics.eu). Sequences were cleaned and contigs were assembled using the software CodonCode Aligner (CodonCode Corporation, Dedlham, MA, USA). The obtained sequence was carefully checked and deposited in the GenBank public database (http://www.ncbi.nlm.nih.gov/genbank/) with the following accession number: PV249064. The individual taxonomic identity was verified by comparison of the COI sequence within the GenBank database using the Blast search tool (https://blast.ncbi.nlm.nih.gov/Blast.cgi). In addition, a Maximum Likelihood tree was built in MEGAX (Kumar et al. 2018), using a General Time Reversible (GTR) model and *S. squatina* COI sequence as outgroup. The dataset COI barcode sequences of *S. aculeata* included sequences from Malta, Senegal, and Turkey obtained from the public repository GenBank and BOLD (www.boldsystems.org) with the following accession numbers: KY909563-KY909575, FN431671, FN431672, KR610532, IRREK940-08. Relationships among the COI haplotypes identified were depicted with the median-joining (MJ) method in Network 10.2 (Fluxusengineering.com) (Bandelt et al. 1999).

Results

The sawback angelshark collected within DCF was caught in April 2023, off the coast of Avola, East Sicily (Fig. 2), during commercial fishing activities targeting cuttlefish (*Sepia officinalis*) by trammel nets, at a depth of 16 m on the sandy bottom, and was found dead. It was a female, measuring 144.7 cm in total length (TL) and weighing 25,020 g. All the morphometric measurements are reported in Table 1. *Squatina aculeata* is an aplacental viviparous species (Capapé et al. 2005), and upon dissection, it was possible to assess the maturity stage according to Follesa and Carbonara (2019), which resulted in a post-reproductive stage (4B), since the uteri were flaccid and large but regenerating as the ovaries were starting to regrow.

It was possible to gather 57 observations of *S. aculeata*—including this one—focusing only on the central Eastern Mediterranean Sea, retrieved from previous studies. From the available data, the species' distribution was drafted according to 45 observations (see Table 1 for further details on location, coordinates, and depths) (Başusta 2002, 2016; Corsini and Zava 2007; Ergenler et al. 2019; Filiz et al. 2005; Giovos et al. 2019; Zava et al. 2020, 2022) between 1997 and 2023, thanks to the availability of the coordinates or the locality of the capture sites (Fig. 2; Table 1). The distribution spans from the central Mediterranean, including Tunisia, Malta, and the eastern and western parts of southern Sicily, to the Aegean Sea and Egypt.

Due to the scarcity of data, the relation total weight (TW)–total length (TL) of the specimens was carried out on

Table 1 Locations, coordinates, depths, year, and reference of the recorded captures of *Squatina aculeata* in the Mediterranean Sea showed in Fig. 2

Location		Coordinates		Depth	Year	Reference
1)	Avola	36.7347	15.1357	16	2024	Current study
2)	Iskenderun Bay	36.41925	35.77662	120–200	1997	Basusta 2002
3)	Bizerta	37.4056	9.6836	120	2007	Zava et al. 4
4)	Bizerta	37.3808	9.7958	75	2007	
5)	Near Zembra MPA	37.0936	10.7436	70	2009	
6)	Malta	35.9598	15.1013	105	2011	
7)	Gulf of Tunis	37.0936	10.7436	50	2013	
8)	Tabarka	37.1061	8.8503	100	2013	
9)	Malta	36.2125	14.6175	137	2014	
10)	Malta	36.0923	14.7102	128	2016	
11)	Off El Alamein, Marsa Matruh city	30.9142	28.9742	55–70	2021	
12)	Between Rhodes Isl. and Turkey	36.5833	28.3333	530	2022	
13)	Saria Isl., Karpathos	35.8326	27.1796	80	2021	
14)	Saria Isl., Karpathos	35.8326	27.1796	80	2021	
15)	Of El Alamein, Marsa Matruh city	30.9142	28.9742	60–70	2021	
16)	Corcelli Isl., Sardinia	41.297	9.4019	40	2021	
17)	Between Rhodes and Turkey	36.7639	25.222	120	2021	
18)	Linosa Isl., Sicily	35.8548	12.8764	35	2022	
19)	SE of Lampedusa (mom)	35.8333	11.9166	90	2011	
20)	SE of Lampedusa (fetus)	35.8333	11.9166	90	2011	
21)	SE of Lampedusa (fetus)	35.8333	11.9166	90	2011	
22)	Egadi Islands, Sicily	38.17531	12.08683	420	2011	Zava et al. 4
23)	Gavdos Isl., South of Crete	34.95	24.20833	500	2015	
24)	Medina Bank, South Ionian Sea	33.6833	15.2	600	2015	
25)	Symi Isl., Aegean Sea	36.47466	27.85566	340–400	2015	
26)	San Vito Lo Capo, Sicily	38.21916	12.83583	545	2015	
27)	Lampedusa Isl., Sicily Channel	35.83333	11.91666	120	2016	
28)	Rhodes Isl.—Aegean Sea	36.6	28.425	550	2016	
29)	Tripoli, South Ionian Sea	33.39233	13.3575	300	2017	
30)	Tripoli, South Ionian Sea	33.39233	13.3575	300	2017	
31)	Gavdos Isl., South of Crete	34.9	24.25033	600	2017	
32)	Gavdos Isl., South of Crete	34.9	24.25033	600	2017	
33)	NE of Rhodes Isl., Aegean Sea	36.521	28.488	500	2017	
34)	off Egadi Islands, Sicily	38.4365	11.55466	159	2018	
35)	Palermo, South Tyrrhenian Sea	38.20524	13.33594	29	2019	
36)	Linosa Isl., Sicily Channel	35.85216	12.87261	40	2019	
37)	Ragusa, South of Sicily	36.80716	14.45933	5	2019	
38)	Linosa Isl., Sicily Channel	35.033333	12.75	90	2020	
39)	Palermo, South Tyrrhenian Sea	38.1885	13.21783	20	2020	
40)	South of Crete	34.96666	24.16666	500	2020	
41)	Gökova Bay	36.96666	27.98333	130	2005	Feliz et al. 2005
42)	North Eastern Med	36.09347	35.28691	415–430	2015	Basusta 2016
43)	Konacık coast, Iskenderun Bay	36.67816	36.11994	47	2019	Ergenler et al. 2019
44)	Marzamemi	36.7258	15.197	70	2017	Giovos et al. 2019
45)	Paradisi - NW coast of Rhodes	36.431	28.153	65–75	2006	Zava and Corsini 2007)

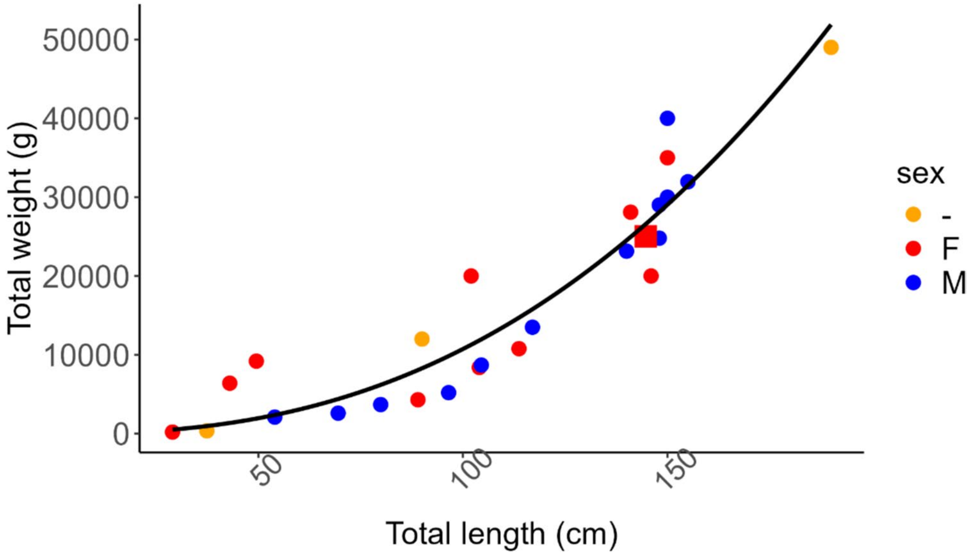


Fig. 3 Total weight (TW) and total length (TL) relationship of 26 specimens of *S. aculeata*. The red square indicates the specimen of this study. All measurements were retrieved from the literature when available

26 animals: 11 females (F), 12 males (M), and 3 specimens without sex (NA), but they had the TL and TW information and thus were included (Fig. 3).

The TW–TL relation for the above 26 specimens resulted in.

$$TW = 0.1156 \cdot TL^{2.4728}; R^2 = 0.8913$$

The value of the estimated parameter b indicated a positive allometric growth.

The stomach was full, and based on Garrido et al. (2008) classification, it scored 3, which means > 50% filled. Stomach total weight, tunic weight, and stomach contents measurements were taken, respectively, 787.09, 203.82, and 583.27 g. In total, eight prey were recognized, all Osteichthyes, and only one prey was recognized at the species level by mandible and maxilla (Table 2 – Fig. 4).

Regarding the vertebrae, 28 transparent bands were counted from the BD to the margin. The CCL is 7.75 mm, the BD is 1.75 mm, and assuming a direct proportionality between CCL and TL, the TL at birth is 218.5 mm (Fig. 5).

A 610-bp fragment of the COI gene was sequenced from the specimen morphologically identified as *Squatina aculeata*. The COI sequence was functional, and no stop codons or NUMTs were found. Blast searching with the GenBank database revealed an identity rate of 99.68% with a query coverage of 100%, corresponding to a COI barcode of *S. aculeata* (GenBank accession number KY909563). The ML tree showed the presence of only two clusters: one with the sequences of the Senegalese samples and the other with all other sequences in the considered Mediterranean data set including our own (Fig. 6).

Only two haplotypes were detected across all sampled individuals. One haplotype was widely shared among multiple sampling locations (Malta, Turkiye, and our sample), whereas the second was less frequent and more geographically restricted to Senegal samples. The haplotype network shows that the two *S. aculeata* haplotypes are only one mutational step apart, whereas the two species, *S. aculeata* and *S. squatina*, are 40 mutational steps apart (Fig. 7).

Table 2 Stomach contents of *Squatina aculeata* in terms of overall prey and percentage

Prey category	Number	%Number
Stomach no empty	1	
Total prey	8	
Osteichthyes	8	100
Sparidae	3	37.5
Diplodus vulgaris	1	12.5

Discussion

The presence of *S. aculeata* in the area between South Sicily, Malta, the northern African coast is well documented, and the Aegean Sea, with numerous observations recorded in the last decades (Başusta 2002; Ergenler et al. 2019; Filiz et al. 2005; Giovos et al. 2019; Ulman et al. 2024; Zava et al. 2020, 2022). Data reported the presence of a pregnant female carrying two near-term fetuses in 2021 in the South-East of Lampedusa Island (Italy), specimens smaller than 50 cm, individuals with total lengths (TL) between 60 and 120 cm, a few females and males measuring 120–140 cm, and many specimens with TL > 140 cm in this area (Giovis et al. 2019; Zava et al. 4, 4). According to Castro (1993), an

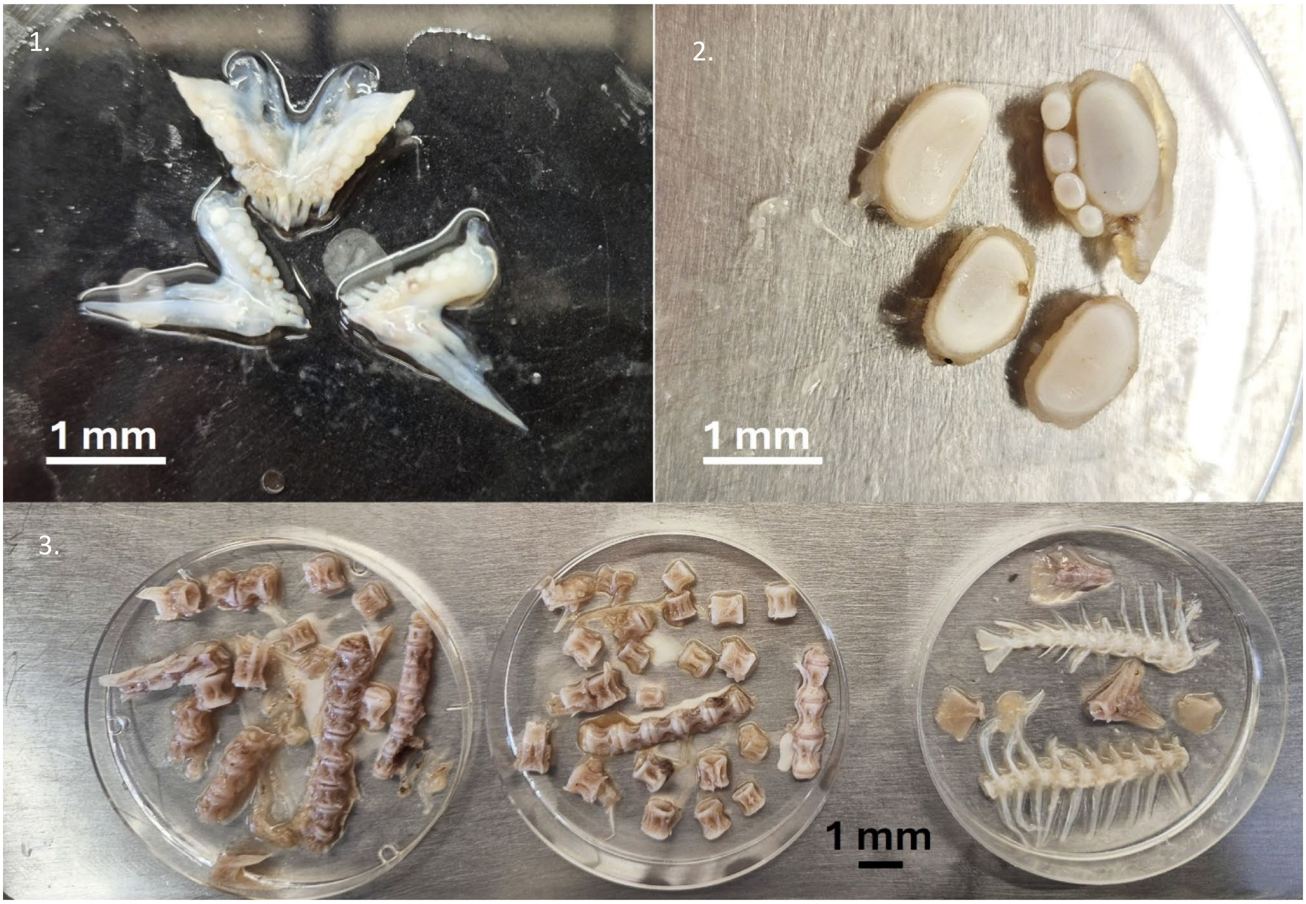


Fig. 4 Stomach content: 1. Close-up of the jaws of *Diplodus vulgaris*; 2. Osteichthyes teeth and 3. vertebrae

area can be considered a breeding and nursery ground when neonates, juveniles, and gravid females are found in a specific location. For *S. aculeata*, the maturity length is approximately 122 cm for males and 143 cm for females (Compagno 1984). Therefore, the data suggests that the abovementioned area could be a potential breeding and nursery ground for this species. It is also worth noting that the specimen discussed in this study was in a post-reproductive stage, which further supports this hypothesis. Although a new definition of the nursery area was suggested by Heupel et al. (2007), according to this, an area could be identified as a nursery when sharks are more commonly encountered in a specific area than others, they tend to remain or return to that area for a long time, and the area is repeatedly used over the years. Nevertheless, the central Eastern Mediterranean Sea seems to be a perfect fit for the species to settle during some life cycle stages. Moreover, according to the most recent findings (in 2015, 2023, 2024), it is evident that the species is present in the Strait of Sicily and the Eastern Mediterranean, highlighting the urgent need for conservation plans and

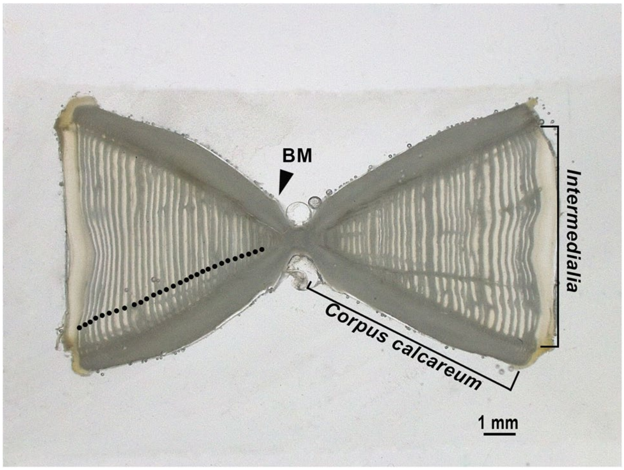
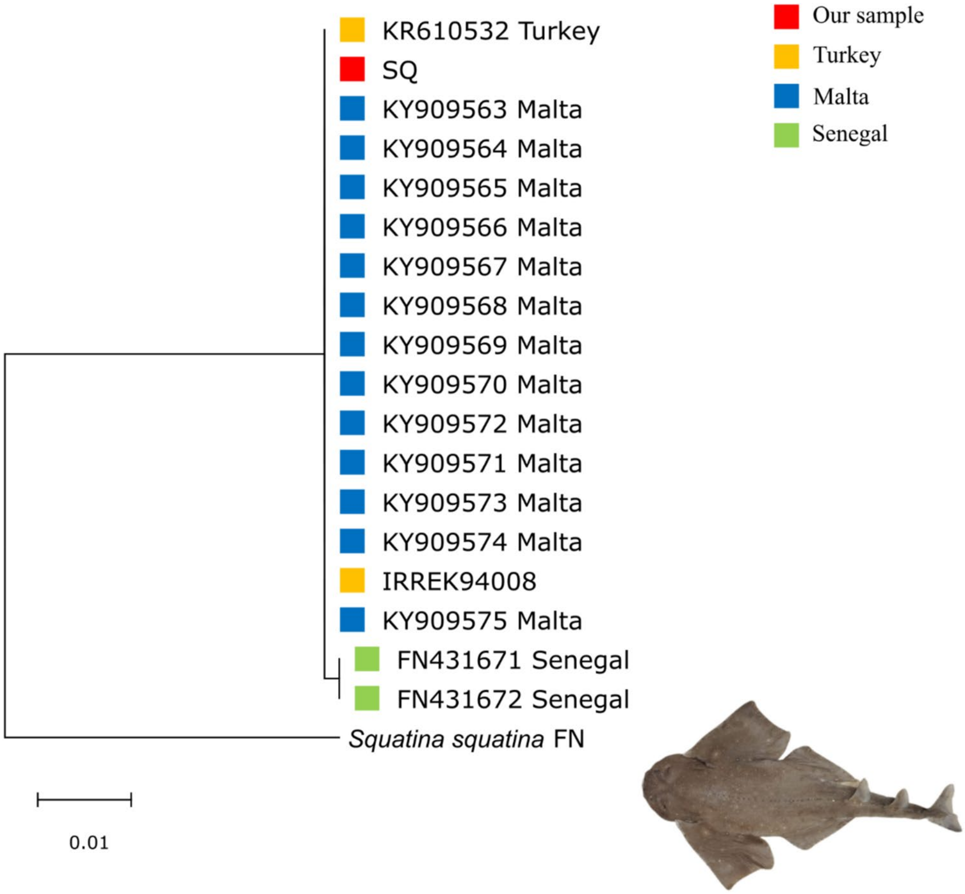


Fig. 5 Thin section of a vertebral centrum of the female of *S. aculeata* analysed in this study (TL = 144.7 cm). The corpus calcareum, intermedialia, the birthmark (BM), and the transparent bands (black circles) are shown

Fig. 6 Maximum likelihood (ML) tree based on the COI sequences of *Squatina aculeata* and constructed using a GTR model calculated in MEGAX



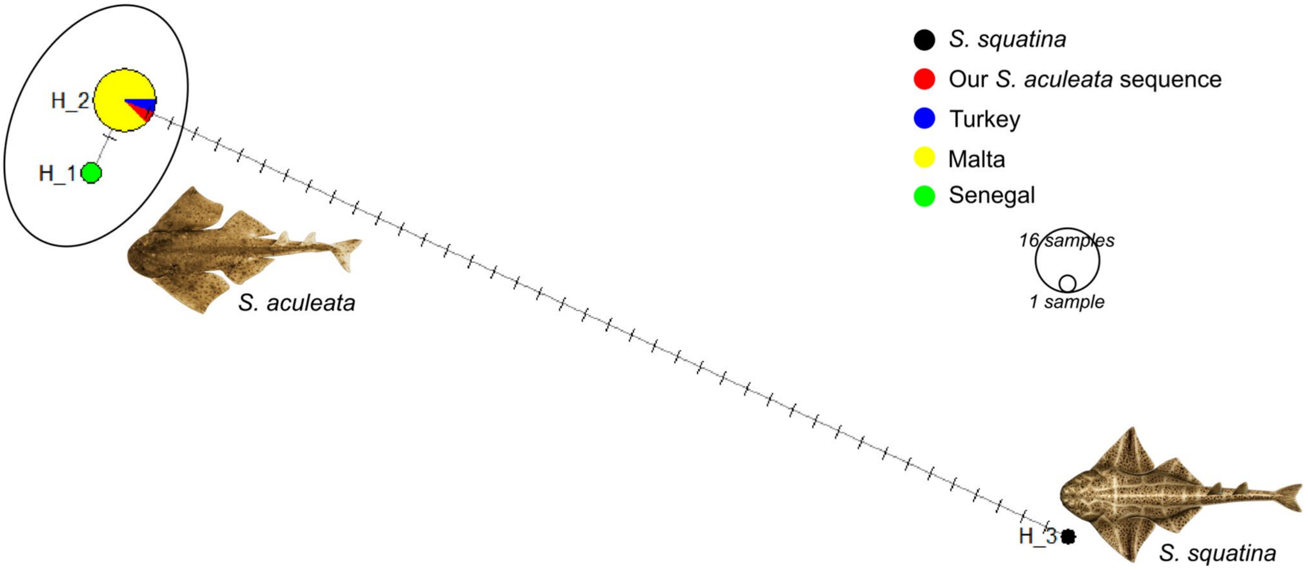


Fig. 7 Median-joining COI haplotype network inferred using NETWORK 10.2.0. Circles represent haplotypes, with circle size proportional to haplotype frequency. Colors indicate sampling locations

monitoring efforts in these areas to ensure the protection and conservation of this species.

The total weight–total length (TW-TL) relation was applicable only for 28 specimens, due to the availability of information. The relationship derived in this study for *S. aculeata* collected in the Mediterranean produced reliable results, with an R^2 value of 0.9059, indicating a strong correlation between length and weight for the data collected in the literature.

S. aculeata's diet comprises small sharks, bony fish, crustaceans, and mollusks (Gordon et al. 2020; Fischer 1987). The stomach contents of the specimen described here had fish bones, including the mandible and maxilla of an individual of *D. vulgaris*. It was not possible to identify any other species, as the contents were highly digested. The presence of *D. vulgaris* is aligned with the depth (around 15 m) at which the specimen was caught and the type of seafloor, specifically a sandy bottom, known as a habitat for the species mentioned above.

Assessing the age of elasmobranchs is challenging due to the absence of hard structures like scales, otoliths, or true bones, which are commonly used in bony fish. Instead, age estimates rely on counting opaque and translucent bands in vertebrae or spines. Techniques described by (Brown and Gruber 3; Cailliet et al. 1992, 2006; Natanson and Cailliet 4) and others have been used, but uncertainties remain regarding the periodicity of band deposition and calcification patterns, which vary among species. The biological mechanisms behind band formation, whether related to age, somatic growth, or life events, are still unknown. Validated age and growth data for elasmobranchs in regions such as the Mediterranean remain scarce (Campana 2014; Carbonara et al. 2020a, b; Kadri et al. 2014). Age studies often use vertebral centra or dermal denticles (Bellodi et al. 2022, 1; Campana 2014), relying on annual deposition of opaque and translucent zones (Panfili et al. 2002). Direct validation methods like mark-recapture and chemical tagging are considered effective (Bellodi et al. 2020; Campana 2001), though their application in elasmobranchs is limited by low calcification and logistical constraints (Björnsson et al. 3). For *S. aculeata*, limited data exist on birth length. Estimates range from 25 to 35 cm (Barrull and Mate 2002; Capapé et al. 2), although recent observations report fetuses as small as 15 cm, but with the yolk sac still attached (Zava et al. 2022). In this study, the vertebral birthmark suggests a birth length of approximately 21.8 cm, indicating variation in reproductive traits and emphasizing the need for further research into the species' life history. Evidence suggests that band deposition may begin before birth. *S. dumeril* specimens under 30 cm have shown 2–6 bands (Baremore 2010), supporting this hypothesis. Similarly, in *S. californica*, band count correlates more strongly with body size than age (Natanson et al. 2018; Natanson and Cailliet 1990).

This study provides the first report of band counts in *S. aculeata*. The vertebrae exhibited 28 bands; however, before assigning an age to these specimens, it is essential to validate the band deposition pattern. In other angel shark species, studies have shown that the number of bands does not necessarily correspond to the actual age of individuals. For example, Baremore et al. (2009) found that for *Squatina dumeril*, the number of bands used as age indicators did not yield realistic estimates of age or length-growth parameters. Similarly, in the Pacific angel shark, *Squatina californica*, band deposition appears to be more closely associated with somatic growth rather than chronological age (Natanson and Cailliet 1990). This preliminary evidence emphasizes the need for continued data collection and, more importantly, the implementation of tagging methods (Baremore et al. 3) to better assess growth rates and validate band deposition as a reliable tool for studying growth in this species.

Molecular analysis based on COI gene sequences identified the specimen examined in this study as *S. aculeata*, confirming the morphological identification. Although several species within the genus *Squatina* can be immediately distinguished using morphological characters, the integration of morphological and molecular data is beneficial for species that are difficult to distinguish due to overlapping traits (Stelbrink et al. 2010). This is the case for (Stelbrink et al. 2) *S. aculeata,* which can be easily confused morphologically with *S. squatina*, as previously reported by Tuney-Kizilkaya and Bengil (2022). These authors used COI and 16S rDNA sequences to assign *S. aculeata* to specimens previously identified as *S. squatina* by morphological analysis (Tuney-Kizilkaya and Bengil 4). In this context, it should be emphasized that correct species identification is of paramount importance, especially for critically endangered species such as *S. aculeata*, to implement correct conservation and recovery plans for the species. However, the very small number of haplotypes observed and the widespread distribution of a single haplotype across different locations, indicate low overall genetic diversity in the dataset and suggest limited genetic differentiation between populations. This finding is consistent with previously reported data from molecular analyses conducted on various species of cartilaginous fish, which are considered a slowly evolving lineage. For example, the slow rate of mitochondrial DNA evolution observed in sharks compared to mammals by Martin et al. (1992) was confirmed for the mitochondrial control region and the COI gene in Chimeriformes by Erk et al. (2025). Similarly, Sendell-Price et al. (2023) found the lowest estimated nuclear mutation rate among vertebrates in epaulette shark, *Hemiscyllium ocellatum*. Further confirmation was found in *Squatina squatina*, where sequencing of four mitochondrial loci revealed exceptionally low genetic diversity, with a high number of haplotypes found in more than 500 common angelsharks examined (Fitzpatrick et al. 2016).

Fishermen and observers on board or at landing grounds make a precious contribution to providing new records; on the other hand, they could provide inaccurate measurements of total length, weight, and sex. Additionally, there is a possibility that fishermen or citizens may misidentify the species, leading to misclassification. To address this, it is essential to train fishermen in proper handling and safe-release techniques, thereby reducing the incidence of capture-induced parturition and improving post-release survival (Ulman et al. 2024). These factors limit the availability and quality of further biological studies. Indeed, despite the bibliographic research conducted to collect as many records as possible, performing any further analyses on biological parameters was impossible. Therefore, there is an urgent need to expand the Mediterranean network for collecting information about angelsharks, to obtain a more accurate understanding of the presence and distribution of *S. aculeata* throughout the Mediterranean Sea, estimate their relative abundance while identifying critical habitats for their life cycle, and eventually implement conservation measures to ensure their survival.

Conclusion

Given the critical status of *S. aculeata*, enhancing data collection and strengthening monitoring efforts are of crucial relevance. Current records are often scarce and reliant on accidental captures, making it difficult to assess population trends and key habitats. Enhancing collaboration among researchers, fishermen, and conservation organizations is necessary to establish a Mediterranean-wide monitoring network. Furthermore, the implementation of targeted conservation measures, including stricter regulations on bottom-fishing activities and the establishment of protected areas, is essential to mitigate bycatch and support the recovery of *S. aculeata* populations. Overall, this study underscores the urgent need for continued research and conservation efforts to prevent the local extinction of *S. aculeata* in the Mediterranean Sea. A more comprehensive approach, integrating ecological, molecular, and fisheries data, is needed to ensure the long-term survival of this critically endangered species.

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Declarations

Conflict of interest The authors declare no competing interests.

Ethical approval This study did not involve the intentional capture or experimental use of live animals. The specimen of *Squatina aculeata* analyzed in this study was obtained as incidental bycatch during authorized commercial fishing activities targeting *Sepia officinalis* using trammel nets off the coast of Avola (Eastern Sicily, Mediterranean Sea). The individual was already dead when the fishing gear was hauled on board, and therefore, no animals were captured or euthanized specifically for the purposes of this research. Sampling was conducted within the framework of the European Union Data Collection Framework (DCF; Regulation EU 2017/1004), which regulates the collection of biological data from commercial fisheries for scientific and management purposes.

Squatina aculeata is a critically endangered species in the Mediterranean Sea, and its capture and trade are prohibited under GFCM Recommendation GFCM/36/2012/3 and its inclusion in Annex II of the Barcelona Convention. The present study relied exclusively on an opportunistically obtained specimen, and no action was carried out with the intent of capturing any specimens of this endangered species. The research activities comply with the ethical guidelines of the COISPA Foundation, which has an Ethics Committee established according to the Italian Ministry of Health regulation (authorization no. 17/2022-UT). Because the analyzed specimen was already dead and obtained as accidental bycatch during routine fisheries monitoring activities, specific ethical approval was not required.

Data availability The data used in this study are included as Supplementary Material.

Author contribution Antonella Consiglio: methodology—morphometric analysis, stomach content analysis, investigation, data curation, writing—original draft; Francesco Tiralongo: methodology, investigation, data curation, writing—original draft, supervision; Andrea Massaro: methodology—vertebrae reading, writing—review and editing; Andrea Bellodi: methodology—vertebrae reading, writing—review and editing; Michele Palmisano: methodology—vertebrae preparation; Cosmidano Neglia: methodology—spatial distribution map; Maria Cristina Follesa: data curation, writing—review and editing; Anna Maria Pappalardo: genetic analyses, writing—review and editing; Giada Santa Calogero: genetic analyses, writing—review and editing; Venera Ferrito: genetic analyses, writing—review and editing; Pierluigi Carbonara: morphometric analysis, stomach content analysis, methodology, investigation, data curation, writing—original draft, supervisor

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